

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2004, 07:06:29 ; Search time 40 Seconds

(without alignments)
1255.629 Million cell updates/sec

Title: US-09-927-458-2

Perfect score: 2754
Sequence: 1 MRLRVRLKRTWPLEVETPE.....DRPPFRPSKGRPTDGLSPM 522Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 263416 seqs, 9621673 residues

Total number of hits satisfying chosen parameters: 263416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries
1: PIR 79: *
2: pir1: *
3: pir2: *
4: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	240.5	8.7	475	2 A86372	53.0K hypothetical
2	187.5	6.8	350	2 H86371	40.0K hypothetical
3	145.5	5.3	547	2 T46366	hypothetical prote
4	128.5	4.7	842	2 T32258	hypothetical prote
5	118	4.3	564	2 H70804	hypothetical prote
6	117.5	4.3	1213	2 A41724	limb deformity (ld
7	117	4.2	403	2 S52796	prplz protein - hu
8	116.5	4.2	915	2 T12586	hypothetical prote
9	116	4.2	4957	2 T03455	ALR protein - huma
10	116	4.2	5262	2 T03454	ALR protein - huma
11	112	4.1	1006	2 G86252	hypothetical prote
12	111.5	4.0	940	2 J60251	FB19 protein - hum
13	111	4.0	1097	2 T49187	hypothetical prote
14	110.5	4.0	551	2 S57447	HPBR1-7 protein -
15	110	4.0	424	2 A54964	spliceosome-associ
16	110	4.0	1468	2 S11515	formin mouse
17	109.5	4.0	742	2 A49672	transcription fact
18	109.5	4.0	772	2 A55004	transcription fact
19	109	4.0	741	2 T46894	probable transcrip
20	109	4.0	1206	2 S24407	formin isoform IV
21	109	4.0	2783	1 A41948	alpha-fetoprotein
22	108	3.9	311	2 T15997	hypothetical prote
23	108	3.9	577	2 T09024	proline-rich prote
24	107.5	3.9	589	2 T29229	hypothetical prote
25	107	3.9	351	1 USB1P1	centromere-binding
26	107	3.9	505	2 A53152	annexin XI - human
27	107	3.9	1257	2 T01020	hypothetical prote
28	106.5	3.9	212	2 S57330	cathelin-like anti
29	106.5	3.9	584	2 G71676	hypothetical prote

30	106	3.8	401	2 T51407	proline-rich prote
31	106	3.8	444	2 E83802	hypothetical prote
32	105.5	3.8	828	2 T06133	hypothetical prote
33	105.5	3.8	882	2 T43250	spindle pole body-
34	105.5	3.8	897	2 A39405	beta-galactosidase
35	105.5	3.8	1465	2 T23056	chromodomain helic
36	105	3.8	502	2 A51197	Wiskott-Aldrich sy
37	105	3.8	715	2 G86239	protein F20B24.6 l
38	104.5	3.8	235	2 A72594	hypothetical prote
39	104.5	3.8	301	2 J01663	hybrid proline-ric
40	104.5	3.8	850	2 J05047	ras GTPase-activat
41	104	3.8	178	2 T36013	probable integrat
42	104	3.8	188	2 D29149	proline-rich prote
43	104	3.8	574	2 H86467	probable transcrip
44	104	3.8	708	2 D96711	hypothetical prote
45	104	3.8	1252	2 D71810	probable type II D

ALIGNMENTS

RESULT 1

A86372
53.0K hypothetical protein F508.33 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C:Accession: A86372

R:Theologis, A.; Eckert, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

Annen, N.F.; Hughes, B.; Hulzar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzalli,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: A86372

A:status: preliminary

A:Molecule type: DNA

A:Residues: 1-475 <STO>

A:Cross-references: UNIPROT:Q9ZUB8; GB:A8005172; NID:G4056460; PIDN:AAC98033.1; GSPDB:GN

C:Genetics:

A:Map position: 1

Query Match	Score	DB 2;	Length
Best Local Similarity	24.5%	Pred. No. 1.2e-09;	475;
Matches	116;	Conservative	89; Mismatches 177; Indels 91; Gaps 20;
1	MRLRVRLKRTWPLEVETPEPTLGLRSHRLSLCTGWSSNRPFTTLNVKPL--TG	58	
3	LRKRHRRETLKLEALAD--TLHDLRRINPTV-----PSSVHSLNRKDELTPS	53	
59	DEETLASGVIGSDILICLLODDIPAPNIPSTSTSESHSSIONNPOSIATSSNOTS	118	
54	PEDTIRSLGLISGLIYPSLE-----AGESNNKLKDSERTVASQSSNOTSVDH	102	
119	QPSDSFGQAQASQGWNDSDMLGPSQNFASIQNNAMARG--TGFPSPRM-----	169	
103	--STGP-----AVDVVPQAKSNP-----TSVED-----PGSDISGMEGPPMDVEQJDM	147	
170	--LCSSEYEGQVPHSLER--LYQADSCDANDALIVLHLMBSGYL--DQGE-----	218	
148	ELAAAGSRKLSPEFLKNTLLKSGDSTELR--TLASVHAWLBSGFVLNAGSDKENFS	206	
219	AKALSMPEKMLSGYKQYHAPLCESSATILTCPLGNLVNATL-----KINNE--	271	
207	KELLTVSRYTLPELIKSKDNTVI--EVSVKFONLPPVVVVGTGCGSSGRVMMNDK	263	
272	RSVRELQLESFICEKEKELGENVANIYKDLQKSLRFLKFDOLVYPLLAFTQALNLP	330	
264	RFVFEVIDLVMDTSTSDS---EGSSSIYREVFMFRVVKXDLIVPLILGICDCKAGL	320	

Matches 109; Conservative 79; Mismatches 197; Indels 151; Gaps 25;

QY 14 LEVETETPTIGHLRSHRLSLCTWGYSSNTFTITLNYDPLTGBEBTLASIGYSGD 73
D 334 MKTPGVDPNYQGGDGHATHSACYHGLRIVQYLE-----NGADQSLASAPFEGAL 386
QY 74 ICLTIDDPDIPAPNIPSSDTEHSHSLQNNQOPSLATSSNOTSQDEQPSDFQGAQSGV 133
D 387 -----RQAGGPTNRPSKVVAIMAINRSDTPSSNAGSNVSLDDQITV-----I 433
QY 134 W-----NDDSLGPSQNFASIODNMAHMGTFYSEPMLCSESVGQ-----VPHSE 184
D 434 WAYERGHDAIVALLKHYAARTVEGD-----VCSEYSSGESSYTPLPSPFG 478
QY 185 TL-----YQADCSGDANDALIVLHLMLTESGY---IPQTEAKALSMPEKMLSGYXQ 237
D 479 RLTLNRDRAIDLQRLRALPAPHLCLAEIPEQESIGSGSGFK-----YKGT 526
QY 238 YMHPLCEGSSATLTCVPLGNLIVNATLKNINIRSVKRLQLLPESFICKELGENVANI 297
D 527 YR-----GKLV-----AVKRYRAM--AFGCKSE---TDWL 551
QY 298 YKDLQKLSRLFKQOLVYVPLAFTROALNLPDVGVLVLEL-----KLIRFLLD 348
D 552 CREVSILSLRAHPNVV---AFVGTSLDPSQFALITEFVNGSLFRRENGEKKNRYMD 607
QY 349 -----VRSVLSLSAVCRDLFTASNDPLLMRFL-----YLRFDNTVRVQDD 391
D 608 PAFRLRLISLDVARGMYRLHESAAKPYIHRDLNHNILIHADGSRVADGESFVQORD 667
QY 392 WKULYRKRNHIQKRESPEK-----GRFVWLBSSTHTIPFYNPPLHPPFPSSRLPQITGG 446
D 668 -ENLTKQPGNLRWMAPEVFSQSGKYRKVDVFSFAVITW--ELHTALPFSHILKPPAAAA 724
QY 447 E--YDQ--RPLTFYVGDV-----ISLIPGGETPSQPPPLPRDPVQPLPGPN 492
D 725 EMTYKRCRPTLP--NQTAPFAHILSLIPQAHNPSS---SRPDIYEIVALLHPR 775

RESULT 5
H70804
Hypochemical protein RV3494c - Mycobacterium tuberculosis (strain H37Rv)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: H70804
R: Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998
A: Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrall, B.G.
A: Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A: Reference number: A70500; MUID:98295987; PMID:9634230
A: Accession: H70804
A: Status: preliminary; nucleic acid sequence not shown; translation not shown
A: Molecule type: DNA
A: Residues: 1-564 <COL>
A: Cross-references: UNIPROT:O53539; GB:AL022022; GB:AL123456; NID:93261554; PIDN:CA11773
A: Experimental source: strain H37Rv
C: Geneticals:
A: Gene: RV3494c

Query Match 4.3%; Score 118; DB 2; Length 564;
Best Local Similarity 25.5%; Pred. No. 1.1;
Matches 51; Conservative 18; Mismatches 51; Indels 80; Gaps 11;

QY 354 SLASVCDLF--TASNDPLMRFLYLDPRDNTVR--VQDTWKELYRKR--HIQKESPK 408
D 343 SYEIPIDMCKTAQNDP-----STVRGRNRPCCFPGKAPVQLCRDR 389
QY 409 GRFVWLBSSTHTIPFYNPPLHPPFPSSRLPQITGGFYDORPTLPYV 457
D 390 G-----YYPVGTNPRGPPIPYGVTEVTDGRNILPPNKP--YIRPGA-----DPRGVPIV 438

QY 458 GDPISLIRPGGEPSSQ-----FPPLRPRF----- 482
D 439 GPPPGGYAGGAPGAPBHQACAPAPPNDNGPPPTSMKPPGIPPPVPRATIPPPP 498
QY 483 -----DPVGPLPGPNPILPG 497
D 499 PEGTGPFGPAPGPOPQASG 518

RESULT 6
A41724
Limb deformity (ld) protein - chicken
C:Species: Gallus gallus (chicken)
C>Date: 04-Mar-1993 #sequence_revision 15-Aug-1997 #text_change 09-Jul-2004
C:Accession: S24286; S38780; A41724
R: Trump, A.; Blundell, P.A.; de la Pompa, J.L.; Zeller, R.
Genes Dev. 6, 14-28, 1992
A: Title: The chicken limb deformity gene encodes nuclear proteins expressed in specific
A: Reference number: A41724; MUID:92112031; PMID:1730407
A: Accession: S24286
A: Status: nucleic acid sequence not shown
A: Molecule type: mRNA
A: Residues: 1-1213 <TRU>
A: Cross-references: UNIPROT:O05858; EMBL:X62681
A: Experimental source: embryo
R: Zeller, R.
submitted to the EMBL Data Library, August 1991
A: Reference number: S38780
A: Accession: S38780
A: Status: preliminary
A: Molecule type: mRNA
A: Residues: 1-885; A', 887-1213 <ZEL>
A: Cross-references: EMBL:X62681; NID:963567; PID:963568
C: Comment: Mutations in this gene affect morphogenesis of both limbs and kidneys.
C: Geneticals:
A: Gene: ld
C: Keywords: nucleus

Query Match 4.3%; Score 117.5; DB 2; Length 1213;
Best Local Similarity 19.4%; Pred. No. 3.7;
Matches 105; Conservative 55; Mismatches 204; Indels 177; Gaps 19;

QY 57 TGDFTLASYGVSGLDILCLTQDDIPRNPSSDTEHSHSLQNNQOPSLATSSN----- 111
D 297 TEDGTTTEIKPRENDLALKLRQPVKKSNTSGITTKSSSEPRASFTLEQJSHLNI 356
QY 112 QTSMDQEPSDFQGAQSGVWMDSMLGPSQNFASIODNMAHMGTFYSEPMLC 171
D 357 DVSKNDEFTQSGAGFGE-----TEDSDGPENVASGQ-----TEPLFP 395
QY 172 SESVGGVPHSLFTLYQADCSGDANDALIVLHL-----MIESGYTQGTGA--KALSMPE 226
D 396 SEETKS-----SPASALDVFKALFTRPKKETPADSELTALIRKRNENE 440
QY 227 KWLKSGVYKQYMHPLCEGSSATLTCVPL-----GNLIVNATLKNINIRSVKRLQL 279
D 441 KESLKAVERSKRKGDPSDKSPDLSPSEDDKTPGLQVWPPPPKNNH----- 491
QY 280 LPESFICKELGENVANIYKDLQKLSRLFKQOLVYVPLAFTROALNLPDVGVLVLEL 339
D 492 -----EVVGVGLKYTEAEYQAAIILHKREHKE-----IETKLSQF 526
QY 340 KLIRFLLDVRSVSL-----SAVCSDLFTASND-----PLLMRFLY 376
D 527 ELRVHNGEVAVSTAQLEETIAHKNELDNKLNRREARDDIGVSTEDDNLPKTYRNC 586
QY 377 LRFDNTVRVQDDTWKELYRKRHIQKESPKGRFVWLBSSTHTI----- 422
D 587 IQTDRETFIKSEENRANVKNQIVPK-----LNISLTFHSISIOGENKDSYVPS 638
QY 423 -----PFYNPPLHPPFPSSRLPQITGGFYDORPTLPYVADPISSLIP 466
D 639 SESVUSCOPKQMLPSPPPPPPPPPPPPP-----PP-----DPPPSDSLSGLVLP 684

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Cy      151  ICNANMAEGCGFAPSEPM-----LCSESYVE----- 176
Dd      3410  -QOOQOVALGPGM--PARKIQHFSSPGALGPTLLTGKQNTVPDPAVSESEATEGSPETHOGG 3467
Cy      177  ---GQPHSLSETLYGSADCSNDADALIVILHMLTBESGYRQ--GTEKALSMPEKXKLS 231
Dd      3468  PLATGTPESATPERGEVKRESLSGDSQLLVQ-----PQPGQSSSIQLQGFPLNLR 3511

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QY 232 GYVKLQ--YMH-----PLCEGSSATLTCVPLGNLIVNATLKINREISVKRLQLP 281
 Db 3519 GQQQQQVSLHTAGGGSHQGLSGSSSSASVDP---HILAQPSVSLGDDPGSMTQNLGLP 3575
 QY 282 ESTICKEKIGENVANITYKDLQKLSRLFKDQVYPLLAFTROALINDVFGVLVPLEKTL 341
 Db 3576 QQPMLEKPMQNTNGP-----QPEKPGPVL---QSGQGLP---GVGIMPTVQGL 3617
 QY 342 RIRFLDVSATLSAVCRDLPFASNDPLIMRFLYLRDRFDNTVVRQDTDMKELYKRI 401
 Db 3618 R---AQLQGVLAKNQRLRLSPQQQQL-----QALLMQRL 3651
 QY 402 QRKESPKGRFVMLLP---SSTHTIPF-----YNP-----LHPPFPFS 436
 Db 3652 QQSQA-----VRQTPPYQEPGTQTSPLQGLGCPQLGFPQGTQPLQELGAGPRFGP 3706
 QY 437 SRL--PGIIGGEYDQRTLPYVG-----DPISLLPGSEPTSPQPPPLRPDPVGLP 489
 Db 3707 PRLPAPGALS-----TGPVLGVPVHTPPSS--PQEPKPSQLPSPSSQLPTEAQLP 3757
 QY 490 GPNPILPGRGGENDRFPFRPSRGRPTDGRLS 520
 Db 3758 PTHPGRPKPGPTLEPP--PGRVSPAAQLA 3786

RESULT 10

ALR protein - human
 C/Species: Homo sapiens (man)
 C/Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
 C/Accession: T03454
 R/Prasad, R.; Znadancov, A.B.; Sedkov, Y.; Bullrich, F.; Druck, T.; Rallapalli, R.; Yano, Oncogene 15, 549-560, 1997
 A/Title: Structure and expression pattern of human ALR, a novel gene with strong homolog
 A/Reference number: Z14954; MUID:97388474; PMID:9247308
 A/Accession: T03454
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-5262 <PRA>
 A/Cross-references: UNIPROT:O14686; EMBL:AF010403; NID:92358284; PIDN:AAC51734.1; PID:92
 C/Genetics:
 A/Gene: ALR
 A/Map position: 12
 C/Superfamily: acute lymphoblastic leukemia protein, ALR type
 C/Keywords: alternative splicing

Query Match 4.2%; Score 116; DB 2; Length 5262;

Best Local Similarity 20.0%; Pred. No. 41;

Matches 102; Conservative 64; Mismatches 181; Indels 164; Gaps 25;

QY 94 EHSLQNEPDLATSNQTSNQMDEQSDSFCQQAQS--GVNND-SYLGPEQNEALS 150

Db 3661 QQQQLQQQQQQQLQQQQQLQQQQQQQQQQQQQQQQQQQQQLNQSRLLSPQQ----- 3714

QY 151 IODNMAEAGTGFYSPM-----LCSESV----- 176

Db 3715 -QQQQCVALLPGM-PAKFLHFSFGALGPTLLTGKQNTVPAYSSATEBSPTHQGG 3772

QY 177 ---GQVPHSLFTLYQADCSNDALIVYIHLIMESGTPQ-GTBARKLSMPEKWKLS 231

Db 3773 PLATGTTESMATEPGEVKPSLQSDQLLVQ-----PQPPQPSLQQLQPPRLP 3823

QY 232 GYVKLQ--YMH-----PLCEGSSATLTCVPLGNLIVNATLKINREISVKRLQLP 281

Db 3824 GQQQQQVSLHTAGGGSHQGLSGSSSSASVDP---HILAQPSVSLGDDPGSMTQNLGLP 3880

QY 282 ESTICKEKIGENVANITYKDLQKLSRLFKDQVYPLLAFTROALINDVFGVLVPLEKTL 341

Db 3881 QQPMLEKPMQNTNGP-----QPEKPGPVL---QSGQGLP---GVGIMPTVQGL 3922

QY 342 RIRFLDVSATLSAVCRDLPFASNDPLIMRFLYLRDRFDNTVVRQDTDMKELYKRI 401

Db 3923 R---AQLQGVLAKNQRLRLSPQQQQL-----QALLMQRL 3956

QY 402 QRKESPKGRFVMLLP---SSTHTIPF-----YNP-----LHPPFPFS 436
 Db 3957 QQSQA-----VRQTPPYQEPGTQTSPLQGLGCPQLGFPQGTQPLQELGAGPRFGP 4011
 QY 437 SRL--PGIIGGEYDQRTLPYVG-----DPISLLPGSEPTSPQPPPLRPDPVGLP 489
 Db 4012 PRLPAPGALS-----TGPVLGVPVHTPPSS--PQEPKPSQLPSPSSQLPTEAQLP 4062
 QY 490 GPNPILPGRGGENDRFPFRPSRGRPTDGRLS 520
 Db 4063 PTHPGRPKPGPTLEPP--PGRVSPAAQLA 4091

RESULT 11

G66292
 hypothetical protein F7H2.17 [imported] - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C/Accession: G66292
 R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiet, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Jensen, N.F.; Hughes, B.; Huizlar, L. Nature 408, 816-820, 2000
 A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, U.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malt, R.; Matzalli, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Iker, M.; Wu, D.; Yu, G.; Frazer, C.M.; Venter, J.C.; Davis, R.W.
 A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A/Reference number: A6141; MUID:21016719; PMID:11130712
 A/Accession: G66292
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-1006 <STO>
 A/Cross-references: UNIPROT:Q9LMQ1; GB:AE005172; NID:9927662; PIDN:AAF2153.1; GSPDB:GMC
 C/Genetics:
 A/Map position: 1

Query Match 4.1%; Score 112; DB 2; Length 1006;

Best Local Similarity 32.7%; Pred. No. 7;

Matches 36; Conservative 6; Mismatches 48; Indels 20; Gaps 3;

QY 406 SPKGRFWLLPSSTHTIPFYFNPPLHPPFPSSRLPGIIGGEYDQRTLPYVGPISLI 465

Db 88 SPENFLFPQP-----DRPPRPPRPPSPRLPP-----PLVSPDPPPL 128

QY 466 PGPETPSQFPPLRPDPVGPLPQPNPILPGRGPN-DRPPFRPSRGRP 514

Db 129 PRPSCPPLMPSPPPLVPSPPPPSPLVSPSPSPSPSPSPSPSPSPSPSPSPSPSPSP 178

RESULT 12

J60291
 FB19 protein - human
 C/Species: Homo sapiens (man)
 C/Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
 C/Accession: J60291
 R/Rotero, A.; Griffo, A.; Carella, M.; Rommens, J.M.; Valentino, M.A.; Roetto, A.; Zelanec Biochem. Biophys. Res. Commun. 250, 565-567, 1998
 A/Title: Cloning of a new gene (FB19) within HLA class I region.
 A/Reference number: J60291; MUID:99003493; PMID:9784381
 A/Accession: J60291
 A/Molecule type: mRNA
 A/Residues: 1-940 <TOR>
 A/Cross-references: UNIPROT:000405; GB:Y13247; NID:92117158; PIDN:CAA73697.1; PID:9211715
 C/Genetics:
 A/Gene: FB19
 A/Map position: 6p21.3

Query Match 4.0%; Score 111.5; DB 2; Length 940;

Best Local Similarity 36.8%; Pred. No. 6.9;

Matches 39; Conservative 6; Mismatches 40; Indels 21; Gaps 6;

QY 424 FYRPHLRHRRPSSRLPPGIIIGSEYDQRTLPYVGDPISSILPGRGETSPQFPLRRPD 483
 DB 643 FPPPGGGMPPGPHGG-PPGVPRLLP PPPPPRGDFFWD---GPGD-PPRGGMGG--- 694
 QY 484 PVGGLPGENPILPGRG-----FNDRFFRPSR-----GRPTDGR 518
 DB 695 --GGGPGGPPHRRGGRGNGNPPPPPPPPFGAGCGSGGPPRGR 738

RESULT 13

T49187
 hypothetical protein MAA21.90 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
 C:Accession: T49187
 R:Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke, K.
 submitted to the Protein Sequence Database, April 2000
 A:Reference number: 225018
 A:Accession: T49187
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1097 <PIE>
 A:Cross-references: UNIPROT:Q9LY69; EMBL:AL163818; GSPDB:GN00061; ATSP:MAA21.90
 A:Experimental source: cultivar Columbia; BAC clone MAA21
 C:Genetics:
 A:Gene: ATSP:MAA21.90
 A:Map position: 3
 A:introns: 106/2; 124/3; 165/3; 198/1; 210/2; 245/3; 265/1; 297/3; 337/3; 352/1; 394/1.

Query Match 4.0%; Score 111; DB 2; Length 1097;
 Best Local Similarity 20.2%; Pred. No. 9.4;
 Matches 111; Conservative 75; Mismatches 218; Indels 146; Gaps 26;
 QY 37 TWG-----SSNRTFTLLNYKDLTDEETLASYGSDLLCLLDD-IPAPN 86
 DB 435 TWGLLKINFEBSGSRKTLISLGLFTLPVAKQAVG---LSSDLNGITLEDTADALD 491
 QY 87 IPSSTDEHSSLQNNQ-----PSLANSSNQTSMQDEPD--SFGQAAGGWNDS 138
 DB 492 LDDNENEAAMFMDGGEFFNNFPKAPDTPVSTAKDMPSTDFTSGEETQEMOEHEE 551
 QY 139 MLGP-----SCNFEASIDN---AMABGTGFP8--EPMCSGS 174
 DB 552 SSDVFNDAIQRALIVGDYKZAVDQITANKADALVIAHG-GTALMBESTREKYLKTS 610
 QY 175 -----VEGVPHSLFTLYOSADCSANDALIVLHILMDESGYIPQGTAKALSMPEKV 228
 DB 611 APYKVVSAVNNDLRSILYTRSHKFWKMTLALC-----TFAGQGEW 653
 QY 229 KLSGVYKIQYHPLCESSSATLTCPVPLGN-LIIVNATLKINNEIRSYKRLQLLPESTICK 287
 DB 654 T-----TLCDALASTL--MAAGNTLAVALCYICAGNDRIVE---TWSRSLAN 696
 QY 288 EKLGENVANIYKDLQKSLRFKQDLYVPLA---FTROALNPDVFGVLP---LELK 340
 DB 697 ERDRSVAEHLQDLMEXK-----LVLAATGNKKFASIOKLFESVABELIAGQLTTA 750
 QY 341 LRIIRLLD-----VNSVLSLAVCRDLPTAS-----NDPLMRFLYLR 378
 DB 751 MKYKVLDSGSLSPELSLIRDRISLSAEPETNTTASNTQPOSTMPYNOEPTQAQPVLA 810
 QY 379 DFRONTVAVDQDWKELEYRKSHIOKESPKGRFVNLPSSTHTIP---FPPNPLHRRPFP 425
 DB 811 NPYNOVOQPTDSDYVQVSH-----PPMOQPTMPPHOAQPAPQDSFTPAT-SSAOP 864
 QY 436 SSR-----LPPGIIGGEYDQRTLPYVGDPISSILPGRGETSPQFPLRRPDVGPPL- 488
 DB 865 SMRTTFVYSTPALAKNADYOQPTMS-----SHSFTGSPNNNAVYPVPGGQVAFSGPSQ 918
 QY 489 --GGNPILP 496
 DB 919 LGQYFNPGRP 928

RESULT 14

S57447
 HPRRII-7 protein - human
 N:Alternate names: HPRRII-4 protein
 C:Species: Homo sapiens (man)
 C:Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 16-Aug-2004
 C:Accession: S57447; S57489
 R:Florschuetz, K.L.
 submitted to the EMBL Data Library, June 1992
 A:Reference number: S57447
 A:Accession: S57447
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-551 <FLB>
 A:Cross-references: UNIPROT:Q16630; EMBL:X67336; NID:g871300; PIDD:CAA47751.1; PID:g871300
 A:Accession: S57489
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-551 <FLB>
 A:Cross-references: EMBL:X67337; NID:g871298; PIDD:CAA47752.1; PID:g871299
 C:Genetics:
 A:introns: 231/3
 C:Superfamily: ribonucleoprotein repeat homology
 F:82-151/Domain: ribonucleoprotein repeat homology <RNM4>

Query Match 4.0%; Score 110.5; DB 2; Length 551;
 Best Local Similarity 31.1%; Pred. No. 3.7;
 Matches 41; Conservative 9; Mismatches 39; Indels 43; Gaps 8;
 QY 408 KGRFVMLPSSSTHTIPFPNPL---HRRPSSRLPPGIIIGSEYDQRTLPYVGDPISS 463
 DB 204 RRRFPAGVPGGDR---PPGAPGPGPPPPPAQQTTP-----RPPGPPGPPPP 250
 QY 464 LIPGGEI---PSQPPPLR-----PRFDVGPL-PPNPILPGRGQFN 502
 DB 251 GPPPPGQVLPPLPAGPPRNRGDRPPPPVLPFGQPPGQP---PLGFLPGRPPPPVPGYGP 307
 QY 503 DRFPFRSGRP 514
 DB 308 G--PPPPQGGP 317

RESULT 15

A54964
 spliceosome-associated protein SAP-49 - human
 C:Species: Homo sapiens (man)
 C:Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
 C:Accession: A54964
 R:Champion-Arnaud, P.; Reed, R.
 Genes Dev. 8; 1974-1983; 1994
 A:Title: The prespliceosome components SAP 49 and SAP 145 interact in a complex implicat
 A:Reference number: A54964; MUID:95047348; PMID:7958871
 A:Accession: A54964
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-424 <CHA>
 A:Cross-references: UNIPROT:Q15427; GB:U35013; NID:g556216; PIDD:AAA60300.1; PID:g556217
 C:Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleoprotein
 F:14-61/Domain: ribonucleoprotein repeat homology <RNM4>
 F:101-169/Domain: ribonucleoprotein repeat homology <RNM2>

Query Match 4.0%; Score 110; DB 2; Length 424;
 Best Local Similarity 32.0%; Pred. No. 2.8;
 Matches 39; Conservative 9; Mismatches 32; Indels 42; Gaps 9;
 QY 430 HRRPSSRLP-PCI-----IG-----GEYDQRTLPYVGDPISSILPQPG 469
 DB 292 HRRPSSRLP-PCI-----IG-----GEYDQRTLPYVGDPISSILPQPG 469
 QY 470 HRRPSSRLP-PCI-----IG-----GEYDQRTLPYVGDPISSILPQPG 469
 DB 292 HRRPSSRLP-PCI-----IG-----GEYDQRTLPYVGDPISSILPQPG 469

Db	346	PPNKGMPRRGPPGSPNKGHPGDMPPHGMKGPPPLMPBHGYTGPPRPPYGYQRGPLPPR	405
Qy	514	PT 515	
Db	406	PT 407	

Search completed: November 16, 2004, 07:21:58
Job time : 44 secs

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OM protein - protein search, using sw model

Run on: November 16, 2004, 06:56:04 ; Search time 202 Seconds

(Without alignments)
1486.859 Million cell updates/sec

Title: US-09-927-458-2

Perfect score: 2754
Sequence: 1 MRLRVRLKRTWFLVEPTE.....DRFPFRPRGRPTDGLSLFM 522

Scoring table: BIOSUM62

Gapop 10.0 , Gapept 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: UniProt_02.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2748	99.8	522	1	FBX7_HUMAN
2	2748	99.8	522	2	CAG30377
3	1977.5	71.8	523	2	Q8K0A5
4	1295	47.0	361	2	Q6Y0L7
5	1295	47.0	361	2	AAP83452
6	1125	40.8	478	2	Q6DE59
7	240.5	8.7	475	2	Q9ZUB8
8	205	7.4	776	2	Q8GZU6
9	187.5	6.8	350	2	Q9ZUB9
10	147	5.3	270	1	PSF1_DROME
11	145.5	5.3	434	2	Q9Y593
12	145.5	5.3	447	2	Q9NT57
13	144	5.2	403	2	Q6PKH7
14	144	5.2	403	2	AH00650
15	144	5.2	447	1	FBX9_HUMAN
16	138.5	5.0	356	2	Q7Z1T2
17	135	4.9	436	2	Q8BVY6
18	135	4.9	437	2	Q8BK06
19	134.5	4.9	1183	2	Q7TSH6
20	134.5	4.9	1209	2	Q6PFR0
21	134.5	4.9	1209	2	AH57592
22	134	4.9	3148	2	Q8H608
23	129	4.7	745	2	Q6Z1Z5
24	129	4.7	745	2	BAD03549
25	128.5	4.6	850	2	Q17055
26	126.5	4.6	431	2	Q7SY92
27	126	4.5	355	1	FX32_HUMAN
28	123	4.5	271	1	PSF1_HUMAN
29	123	4.5	936	2	Q8GR77
30	122	4.4	953	2	Q6MB50
31	122	4.4	953	2	CAF24199

32	120.5	4.4	888	2	Q6P9Q5	Q6P9Q5 mus musculu
33	120.5	4.4	888	2	AH60652	AH60652 mus muscu
34	120.5	4.4	911	2	Q8CIE2	Q8CIE2 mus musculu
35	120.5	4.4	925	2	Q8NF64	Q8NF64 homo sapien
36	120	4.4	271	2	Q8BHL8	Q8BHL8 m mus muscu
37	120	4.4	684	1	CC04_CANAL	P53699 candida alb
38	120	4.4	1255	2	Q9R2J6	Q9R2J6 plasmid col
39	119	4.3	271	2	Q8C0G9	Q8C0G9 mus musculu
40	119	4.3	287	2	Q95UG5	Q95UG5 babesia bov
41	119	4.3	844	2	Q9R2J5	Q9R2J5 plasmid col
42	118	4.3	442	2	Q9VG61	Q9VG61 drosophila
43	118	4.3	564	2	Q53539	Q53539 mycobacteri
44	118	4.3	564	2	Q7WMD7	Q7WMD7 mycobacteri
45	117.5	4.3	503	1	WALP_HUMAN	Q43516 homo sapien

ALIGNMENTS

RESULT 1

ID	FBX7_HUMAN	STANDARD	PRT	522 AA.
AC	Q9Y311, Q96HM6, Q9UF21, Q9UKT2;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	F-box only protein 7			
GN	Name=FBX07; Synonyms=FBX7;			
OC	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE OF 41-522 FROM N.A.			
RX	MEDLINE=20003060; PubMed=10531035;			
RA	Cenciarelli C., Chaur D.S., Guaravaccaro D., Parks W., Vidal M.,			
RA	Pagano M.;			
RT	"Identification of a family of human F-box proteins";			
RL	Curr. Biol. 9:1177-1179(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=2039565; PubMed=10945468; DOI=10.1038/990031;			
RA	Dunham I., Hunt A.R., Collins J.E., Bruskewich R., Beare D.M.,			
RA	Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babage A.K.,			
RA	Baggaley C., Bailey J., Barlow K.F., Bates K.N., Beasley C.P.,			
RA	Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,			
RA	Burhill W.D., Burton J., Carter C., Carter N.P., Chen Y., Clark G.,			
RA	Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,			
RA	Conroy D., Cordy N.R., Coville G.J., Cox A.V., Davis U., Dawson E.,			
RA	Dhand P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,			
RA	Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,			
RA	Gilbert J.G.R., Goward M.E., Graffham D.V., Griffiths M.N.D., Hall C.,			
RA	Hall R.E., Hall-Famlyn G., Heathcote R.W., Ho S., Holmes S.,			
RA	Hunt S.E., Jones M.C., Kerhaw J., Kimberley A.M., King A.,			
RA	Laid G.K., Langford C.P., Leverisa M.A., Lloyd C., Lloyd D.M.,			
RA	Marlyn I.D., Mashreghi-Mohammadi M., Matthews U.H., Mccann O.T.,			
RA	McClay J., McLaren S., McMurtry A.A., Milne S.A., Mortimore B.U.,			
RA	Odeh C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,			
RA	Phillips S.H., Plumb R.W., Ramsey H., Ramsey Y., Rogers L., Rose M.T.,			
RA	Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,			
RA	Seatonland C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,			
RA	Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Wiley D.L.,			
RA	Williams L., Williams S.A., Williamson H., Wilner T.E., Wilning L.,			
RA	Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,			
RA	Winoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudo H.,			
RA	Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,			

FT	CONFLICT	41	41	S -> M (in Ref. 1)
FT	CONFLICT	79	79	Q -> H (in Ref. 1) .
FT	CONFLICT	84	84	A -> P (in Ref. 1) .
FT	CONFLICT	115	115	M -> I (in Ref. 1 and 4) .
FT	CONFLICT	169	169	M -> L (in Ref. 1) .
FT	CONFLICT	224	224	M -> L (in Ref. 1) .
FT	CONFLICT	241	241	P -> H (in Ref. 1) .
FT	CONFLICT	328	328	D -> N (in Ref. 1) .
FT	CONFLICT	413	413	M -> L (in Ref. 1) .
FT	CONFLICT	475	475	F -> L (in Ref. 1) .
SO	SEQUENCE	522 AA,	58502 MW,	CAB5E0A074287A CRC64;
<hr/>				
Query Match				
Best Local Similarity 99.8%; Score 2748; DB 1; Length 522;				
Matches 521; Conservative 0; Mismatches 1; Indels 0; Gaps 0				
<hr/>				
QY	1 MLRLVRLKRTPTLPTEVPETPEPTGLGHLRSRLSLCTWGYSSNTRFITTLYNDPLTGDDE	60		
DB	1 MLRLVRLKRTPTLPTEVPETPEPTGLGHLRSRLSLCTWGYSSNTRFITTLYNDPLTGDDE	60		
QY	61 ETLASGIYSVDLLICLILODDIPAPNPISSTDSHSSLONNEOPSLATSSNOTSMODEOP	120		
DB	61 ETLASGIYSVDLLICLILODDIPAPNPISSTDSHSSLONNEOPSLATSSNOTSMODEOP	120		
QY	121 SBSFGQAAGSGVMWDSDMLSPGNFEASTODNAHAKEGTGPSPBPMCSBSVEGOYP	180		
DB	121 SBSFGQAAGSGVMWDSDMLSPGNFEASTODNAHAKEGTGPSPBPMCSBSVEGOYP	180		
QY	181 HSLETTYGSADSCDNDALIVLHILMLESSEYIQGTAEARLASMPERKXLSGVYKLQYNH	240		
DB	181 HSLETTYGSADSCDNDALIVLHILMLESSEYIQGTAEARLASMPERKXLSGVYKLQYNH	240		
QY	241 PLCEGSSATLTTPVPGNLIVNNATIKINNEFRSKYRQLLPESFTCKEKIGENVANNIYKD	300		
DB	241 PLCEGSSATLTTPVPGNLIVNNATIKINNEFRSKYRQLLPESFTCKEKIGENVANNIYKD	300		
QY	301 LGCLSLSPFDOLVYLAFTRQALNLPVFGLIVLPLELKIRIFRLLDVRSVLSLAVCR	360		
DB	301 LGCLSLSPFDOLVYLAFTRQALNLPVFGLIVLPLELKIRIFRLLDVRSVLSLAVCR	360		
QY	361 DLFETASNDPLMRFLYLRDPFRDITVRVODTDWKELRYKRKHIOREKSRKGFWMILPSSH	420		
DB	361 DLFETASNDPLMRFLYLRDPFRDITVRVODTDWKELRYKRKHIOREKSRKGFWMILPSSH	420		
QY	421 TTFEYFNPLPHPPPPSSRLPPIITIGEGVDQRPTLPVYGDPISLILPQGGTPSQCFPLRP	480		
DB	421 TTFEYFNPLPHPPPPSSRLPPIITIGEGVDQRPTLPVYGDPISLILPQGGTPSQCFPLRP	480		
QY	481 RPDVPGPLPGPNLIPGRGCPDRPFPPSPSRRPTDGLSLFM	522		
DB	481 RPDVPGPLPGPNLIPGRGCPDRPFPPSPSRRPTDGLSLFM	522		
<hr/>				
RESULT 2				
ID	CAG30377	PRELIMINARY;	PRT;	522 AA.
AC	CAG30377;			
DT	01-JUN-2004 (T-EMBLrel. 27, Created)			
DT	01-JUN-2004 (T-EMBLrel. 27, Last sequence update)			
DT	01-JUN-2004 (T-EMBLrel. 27, Last annotation update)			
DE	FBXO7 protein.			
GN	FBXO7.			
OS	Homo sapiens (Human).			
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Cole Collins J.E., Wright C.L., Edwards C.A., Davis M.P., Grinstead U.A.,			
RA	Cole C.G., Goward M.E., Aguado B., Maliya M., Mokrab Y., Huckie E.J.,			
RA	Beare D.M., Dunham I.,			
DR	Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.			
DR	EMBL, CR546491; CAG30377.1; -.			

SQ SEQUENCE 522 AA; 58502 MW; CAESE70A0747287A CRC64;
 Query Match 99.8%; Score 2748; DB 2; Length 522;
 Best Local Similarity 99.8%; Pred. No. 2e-175;
 Matches 521; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRLVRLIKRTWPLEVEPTETPTLGHLSRLSLCTWGYSSNTRFTITLNYKPLTIDE 60
 DB 1 MRLVRLIKRTWPLEVEPTETPTLGHLSRLSLCTWGYSSNTRFTITLNYKPLTIDE 60
 QY 61 ETLASVIGSGDLICLLODDIPAPNIPSSDSEHSSLONNQPSLATSSNOTSMQDEOP 120
 DB 61 ETLASVIGSGDLICLLODDIPAPNIPSSDSEHSSLONNQPSLATSSNOTSMQDEOP 120
 QY 121 SDSFGQAAQSGVWVNDSDMLGPSQNFPEAESIQDNAHAEGTGFYPSSEPMCSSEVGGVP 180
 DB 121 SDSFGQAAQSGVWVNDSDMLGPSQNFPEAESIQDNAHAEGTGFYPSSEPMCSSEVGGVP 180
 QY 181 HSLFTLYQSADCSNDALIVLHLMLESGYIPQGTBAKALSMPEKMKLSGYKLYQYMH 240
 DB 181 HSLFTLYQSADCSNDALIVLHLMLESGYIPQGTBAKALSMPEKMKLSGYKLYQYMH 240
 QY 241 PLCEGSSATLTCVPLGNLIVNATLKINNEIRSVYKRLQLPESPTCKEKLGENVANITYCD 300
 DB 241 PLCEGSSATLTCVPLGNLIVNATLKINNEIRSVYKRLQLPESPTCKEKLGENVANITYCD 300
 QY 301 LQKLSRLFKQQLVYPLIAFTROALNPDVFGVLVPLLEKLRIIFRLIDVRSVLSAYCR 360
 DB 301 LQKLSRLFKQQLVYPLIAFTROALNPDVFGVLVPLLEKLRIIFRLIDVRSVLSAYCR 360
 QY 361 DLFTASNDPLMLRLYLDRDNTVRYQDMDKELVYKRIQKESKGFVWLLSSSTH 420
 DB 361 DLFTASNDPLMLRLYLDRDNTVRYQDMDKELVYKRIQKESKGFVWLLSSSTH 420
 QY 421 TIFPYPNLHPRPPSSRLPPGIIGGEYDQRTLPHYGDPISLILPGGPTPSQFPPLRP 480
 DB 421 TIFPYPNLHPRPPSSRLPPGIIGGEYDQRTLPHYGDPISLILPGGPTPSQFPPLRP 480
 QY 481 RPDVPGLPGPNPILPGRGPNDRFPPRPSRGRPTDGRLSFM 522
 DB 481 RPDVPGLPGPNPILPGRGPNDRFPPRPSRGRPTDGRLSFM 522

RESULT 3
 O8K0A5 PRELIMINARY; PRT; 523 AA.
 ID O8K0A5; AC O8K0A5;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE F-box only protein 7.
 GN Name=FbxO7;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Liver;
 RX MEDLINE=23388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,
 RA Diatchenko L., Marziani K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mollari S.J.,
 RA Bosak S.A., McWeney P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Snechenko Y., Bouffard G.G.,

RA Blakesley R.M., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywicki M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Maira M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Liver;
 RA Strausberg R.,
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC032153; AAH32153.1; -
 DR MGI; MGI:1917004; FbxO7.
 DR InterPro; IPR001810; F-box.
 DR Pfam; PF00646; F-box; 1.
 DR PROSITE; PS50181; FBOX; 1.
 SQ SEQUENCE 523 AA; 57634 MW; ABFD250070C1FEB5 CRC64;
 Query Match 71.8%; Score 1977.5; DB 2; Length 523;
 Best Local Similarity 72.5%; Pred. No. 7e-124;
 Matches 380; Conservative 56; Mismatches 85; Indels 3; Gaps 3;

QY 1 MRLVRLIKRTWPLEVEPTETPTLGHLSRLSLCTWGYSSNTRFTITLNYKPLTIDE 60
 DB 1 MRLVRLIKRTWPLEVEPTETPTLGHLSRLSLCTWGYSSNTRFTITLNNKALITIDE 60
 QY 61 ETLASVIGSGDLICLLODDIPAPNIPSSDSEHSSLONNQPSLATSSNOTSMQDEOP 120
 DB 61 ETLASVIGSGDLICLLODDIPAPNIPSSDTHSSLONNQPSLATSPOTINIPDQOG 120
 QY 121 SDSFGQAAQSGVWVNDSDMLGPSQNFPEAESIQDNAHAEGTGFYPSSEPMCSSEVGGVP 180
 DB 121 SDSFGQAAQSGVWVNDSDMEGPSQNFPEAESIQDAKMEVSGFHLPEMLCNETEDQVP 180
 QY 181 HSLFTLYQSADCSNDALIVLHLMLESGYIPQGTBAKALSMPEKMKLSGYKLYQYMH 240
 DB 181 HSLFTLYQSAGCSNIDALIVLHLMLESGYIPQGTETKAVTEPMKSSGVVYLQYTH 240
 QY 241 PLCEGSSATLTCVPLGNLIVNATLKINNEIRSVYKRLQLPESPTCKEKLGENVANITYK 299
 DB 241 PLCEGSGFVLTCVPLGNLIIINATIKVNGCIKAKSVQLOQSGYVAGVGEGBAAKYK 300
 QY 300 DLQKLSRLFKQQLVYPLIAFTROALNPDVFGVLVPLLEKLRIIFRLIDVRSVLSAYC 359
 DB 301 DLKLSRLFKQQLVYPLIAFTROALNPDVFGVLVPLLEKLRIIFRLIDVRSVLSAYC 360
 QY 360 RDLFTASNDPLMLRLYLDRDNTVRYQDMDKELVYKRIQKESKGFVWLLPEST 419
 DB 361 HDLFTASNDPLMLRLYLDRDNTVRYQDMDKELVYKRIQKESKGFVWLLPEST 419
 QY 420 HTIFPYPNLHPRPPSSRLPPGIIGGEYDQRTLPHYGDPISLILPGGPTPSQFPPLRP 478
 DB 420 HTIFPCPIPVYPAVLPFSLPPGIIGGEYDERLIPSGVDPVSLIPREBELGQFPL 479
 QY 479 RPRPVPVGLPGPNPILPGRGPNDRFPPRPSRGRPTDGRLSFM 522
 DB 480 RPRPVPVGLPGPNPILPGRGPNDRFPPRPSRGRPTDGRLSFM 523

RESULT 4
 O6Y0L7 PRELIMINARY; PRT; 361 AA.
 ID O6Y0L7; AC O6Y0L7;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE F-box only protein 7 (Fragment).
 GN Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;

```

RN [1]
RP SEQUENCE FROM N.A.
RA Emara M.G., Kim H.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY194289; AAP83452.1; JOINED.
DR EMBL; AY194288; AAP83452.1;
DR InterPro; IPR001810; F-box.
DR Pfam; PF00646; F-box; 1.
DR SMART; SM00256; FBOX; 1.
DR PROSITE; PSS0181; FBOX; 1.
FT NON_TER
SQ SEQUENCE 361 AA; 40110 MW; 51C54C0292833884 CRC64;

Query Match 47.0%; Score 1295; DB 2; Length 361;
Best Local Similarity 65.6%; Pred. No. 1,9e-78;
Matches 246; Conservative 47; Mismatches 62; Indels 20; Gaps 4;

153 DNAAAGCTGFPYSEPMKCSSEVGVPHSLETLTYSADCSNDALIVLHILMLESGY 212
2 EDVLEEGTGSYPSEPMKCSSEADGELPHSLEVLITSAECTSADALIVLHILMLETGY 61
213 IPGTEAKALSMPEKMKLSGVYKLYMHPLECGSSATLTCVPLGNLIVNATLKINNEIR 272
62 VPQTEAKAYSMPEKMKNGNYKLYTHPLCEBSAGLTCVPLGDLVAINATLKINREIK 121
273 SVKRLQLLPESFICKKLGENVANIYKDLQKLSLFFDQVYPLATRQALNLPDVFGL 332
122 GVKRIQLLPASFVCFQE-PEKVAGVYKDLQKLSLFFDQVYSLAARQALNLPDVFGL 180
333 VVLELEKLRIFRLIDVRSVSLSAVCRDLFTASNDPLMRFLYLRFDRNTAVQDTDW 392
181 VVLELEKLRIFRLIDVRSVSLSAVCRDLFTASNDPLMRFLYLRFDRNTAVQDTDW 227
393 KELYKRIHQKESPKRFVWLLPSSTHTTIPFYNPPLHPDPSPSRUP-----PGIIGE 447
228 SELYKKLQKKKEALRWKH-MFLPPTPIPIPHNPFPSPFPNPSPNPPIYDPMWIGE 286
448 YDQRTLPYVGDPISSLLPGSGETPSQPPRPPFPDVPGLPGNPPLIPGRCGNDPFP 507
287 YGERPTLLYIGDPIINSLLPGGEAPGQPPPRPHFDIGSLPGANPTLPGAGSDPFP 346
508 RPSRGRPTDGRLSFM 522
347 RPSRGRPTDVRRAFI 361

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RESULT 5
AAP83452 PRELIMINARY; PRT; 361 AA.
ID AAP83452;
AC 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE F-box only protein 7 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinoptera; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Emara M.G., Kim H.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY194289; AAP83452.1; JOINED.
DR EMBL; AY194288; AAP83452.1;
DR InterPro; IPR001810; F-box.
DR Pfam; PF00646; F-box; 1.
DR SMART; SM00256; FBOX; 1.
DR PROSITE; PSS0181; FBOX; 1.
FT NON_TER
SQ SEQUENCE 361 AA; 40110 MW; 51C54C0292833884 CRC64;

Query Match 47.0%; Score 1295; DB 2; Length 361;
Best Local Similarity 65.6%; Pred. No. 1,9e-78;
Matches 246; Conservative 47; Mismatches 62; Indels 20; Gaps 4;

153 DNAAAGCTGFPYSEPMKCSSEVGVPHSLETLTYSADCSNDALIVLHILMLESGY 212
2 EDVLEEGTGSYPSEPMKCSSEADGELPHSLEVLITSAECTSADALIVLHILMLETGY 61
213 IPGTEAKALSMPEKMKLSGVYKLYMHPLECGSSATLTCVPLGNLIVNATLKINNEIR 272
62 VPQTEAKAYSMPEKMKNGNYKLYTHPLCEBSAGLTCVPLGDLVAINATLKINREIK 121
273 SVKRLQLLPESFICKKLGENVANIYKDLQKLSLFFDQVYPLATRQALNLPDVFGL 332
122 GVKRIQLLPASFVCFQE-PEKVAGVYKDLQKLSLFFDQVYSLAARQALNLPDVFGL 180
333 VVLELEKLRIFRLIDVRSVSLSAVCRDLFTASNDPLMRFLYLRFDRNTAVQDTDW 392
181 VVLELEKLRIFRLIDVRSVSLSAVCRDLFTASNDPLMRFLYLRFDRNTAVQDTDW 227
393 KELYKRIHQKESPKRFVWLLPSSTHTTIPFYNPPLHPDPSPSRUP-----PGIIGE 447
228 SELYKKLQKKKEALRWKH-MFLPPTPIPIPHNPFPSPFPNPSPNPPIYDPMWIGE 286
448 YDQRTLPYVGDPISSLLPGSGETPSQPPRPPFPDVPGLPGNPPLIPGRCGNDPFP 507
287 YGERPTLLYIGDPIINSLLPGGEAPGQPPPRPHFDIGSLPGANPTLPGAGSDPFP 346
508 RPSRGRPTDGRLSFM 522
347 RPSRGRPTDVRRAFI 361

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RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S., Strassberg R.;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC077283; AAF7283.1;
 KM Hypothetical protein.
 SO SEQUENCE 478 AA; 53251 MW; 8C12F0132C1873F CRC64;
 Query Match 40.8%; Score 1125; DB 2; Length 478;
 Best Local Similarity 47.5%; Pred. No. 6.5e-67;
 Matches 251; Conservative 74; Mismatches 147; Indels 56; Gaps 14;
 QY 1 MRLRLVRLKRTWPLEVETEPTEPTLGHLSRLSLCTWGSNTPTITLNYKDTGDE 60
 DB 1 MKLRVRVRKQTSRLTEAEQPTLGDRLSKLSVTLPSLGSATHTPITLNGDALTEQ 60
 QY 61 ETLASVYIGVDLICTLLOD--DIPAPNIPSTPSEHS--QNNQPSLATSSNQTSMODE 118
 DB 61 TTLESATIIISGDLIVLLPPSPQAPAPRERD-PRCPLEDPQP-----CSTANK 111
 QY 119 QPSDSFGQAAGSGVWVNDMSNLGPGSFQFEASIQDNAMAEGTGFYPS-EPMLCSSEV 177
 DB 112 RP-----KGADNEGA-----GAMPQAEASPSLDVAM-EGQLSGPAWEVMLCSBAVDG 159
 QY 178 QVPHSLTETLYQASDCSDANDALTYLHLMLESGYIPQGTAEALSMPEKMSGYVYKQ 237
 DB 160 KIPHSLEVLVQTASCSASDAFVIVHLMLEGTGLKGETALCPWRMRSGAVRLH 219
 QY 238 YMAPLCEGSSATLTCVPLGNLIVNATLKTINNEIRSYKRLQILPESFICEKLGENVANI 297
 DB 220 YTHPLCAEVSATLVCPLMGKLVINATMTKINSEKSKYRKQLLTNSYISPEPDNNVASG 279
 QY 298 YKDLQKSLRFLKQOLVPLAFTROALNPDVGLVTLPELKLRIFFLIDVSGVSLGA 357
 DB 280 YKDLQKSLSGFQKQVAPPLAAARQVNLDPVGLVLPPELKLRIFFLIDISLINTLSA 339
 QY 358 VCRDLFTASNDPLIMRELYLRFDNDTVRVQDTMKELYKRIORKESEPKGSFV---ML 414
 DB 340 TCKELALADTDPSLMRFLCIRDFRNLSPRLGTDWKKLYEKRKQKMD--RNFVVRQEL 397
 QY 415 LPSTGATLTPYPNPLAHPRPSSSLPPGIIIGGEYDQRPILPYGDPISLIPGSGTSP 474
 DB 398 PPRNAHYPPYPPN-VFP---PDINYPPIIGIGDYDQRPFPPIV-----NPTH 440
 QY 475 FPLPRPFDPVGLPGNPILPGSGGNDRFPSPSGRPTDGLSPM 522
 DB 441 LNP-----FKVTLTPSENDPSIPSSG-----LRPSRGRLDIRRGFI 478
 RESULT 7
 Q9ZUB8 PRELIMINARY; PRT; 475 AA.
 AC Q9ZUB8;
 DT 01-MAY-1999 (TEMBLrel. 10, Created)
 DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)
 DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
 DE F508_33 protein (At1g23780/F508_31).
 GN Name=F508_33;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Vysotskaja V.S., Schwartz J.R., Yu G., Toriumi M., Liu S., Lenz C.,
 RA Li J., Kremensskaja I., Luross T., Altafi H., Gonzalez A., Araujo R.,
 RA Buehler E., Comin L., Conway A.B., Dunn P., Hansen N., Hultzer L.,
 RA Kim C., Palm C.J., Rowley D., Shinn P., Walker M., Davis R.W.,
 RA Ecker J.R., Federspiel N.A., Theologis A.;

RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Theologis;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Barth J.,
 RA Bower U., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
 RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Natusaka M.,
 RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
 RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.,
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Shin P., Chen H., Cheuk R., Kim C.J., Bower U., Carninci P.,
 RA Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hayashizaki Y.,
 RA Hsuan Y.W., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Natusaka M.,
 RA Nguyen M., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M.,
 RA Southwick A., Tang C.C., Toriumi M., Wallender E.X., Wong C., Wu H.C.,
 RA Yamada K., Yu G., Yuan S., Shinozaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.,
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC005990; AAC98033.1;
 DR EMBL: AY045291; AAK83633.1;
 DR EMBL: AY145929; AAN31083.1;
 DR PIR: A86372; A86372.
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR002052; N6_Mtase.
 DR InterPro: IPR008945; Skp1_Skp2.
 DR Pfam: PF00646; F-box; 1.
 DR SMART: SM00256; FBOX; 1.
 DR PROSITE: PS00181; FBOX; 1.
 DR PROSITE: PS00092; N6_Mtase; UNKNOWN 1.
 DR SEQUENCE 475 AA; 52947 MW; D068CFF15448FC3 CRC64;
 Query Match 8.7%; Score 240.5; DB 2; Length 475;
 Best Local Similarity 24.5%; Pred. No. 9.5e-08;
 Matches 116; Conservative 89; Mismatches 177; Indels 91; Gaps 20;
 QY 1 MRLRLVRLKRTWPLEVETEPTEPTLGHLSRLSLCTWGSNTPTITLNYKDTGDE 58
 DB 3 LRLRHEHRETLKELADAD-TLHDLRRINPTV-----PSSVHLSLRKDELIIPS 53
 QY 59 DEETLASVYIGVDLICTLLODDIPAPNIPSTPSEHS--QNNQPSLATSSNQTSMODE 118
 DB 54 PEDTLRSGLISGDLIYPSLR-----AGESNMKRLDSSTVVAQSSESNQTSVAD- 102
 QY 119 QPSDSFGQAAGSGVWVNDMSNLGPGSFQFEASIQDNAMAE--TGFPSPSPM----- 169
 DB 103 --SIGF-----AEVDVPPQAKSNP-----TSVED-----PEGDISGMGPPEMDVEQLDM 147
 QY 170 --LCESEYEGVPHSLFT--LYQADCGSDANDALIVLHLMLESGYT--DQGT----- 218
 DB 148 ELAAGSRLESEPFPLKNIILEKSGDTSLET-TTALSVAHVMLESGFVLNHGSDKFNFS 206
 QY 219 AKALSMPEKWLISGYKQVNHPLCEGSSATLTCVPLGNLIVNATL-----KINNE-- 271
 DB 207 KELTASISRTILPELIKQNTNTT---ESVVKFQNLSPVVVVVGVIGSSGRVHANNIDK 263
 QY 272 -RSYRLQLPESFICEKLGENVANIYKDLQKSLRFLKQOLVPLAFTROALNPDV 330
 DB 264 RRFVVIDLVMDTSTNDE--EGSSIRYEVFMFRMWKDLVLPILIGICDXAGLEPP 320
 QY 331 GLVLPFLKRLRIFLLDVRSVLSISANCRLDFTASNDPLMRPLYLRFDFDNTVYV--Q 388
 DB 321 CILMRPLTKLILLELGVASIGNACVCTMRVLIASNDIMKQCLAEVNNFVVTAGD 380
 QY 389 DTDWK-----ELVYKRRIORKESEPKGRFVMLPSSHTPTIP 424

Db 381 SVNKKARFATFWKQKOLAASDTFWRONOLGRBNISTGRSGIRFFRILGDPF 433

RESULT 8

Q8GZV6 PRELIMINARY; PRT; 776 AA.

AC Q8GZV6; 01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DE Hypothetical protein O1017C11.10.
 GN Name=O1017C11.10;
 OS Oryza sativa (Japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 CC Eubacteriales; Oryzaeae; Oryza.
 NCBI_TaxID=39947;

RP SEQUENCE FROM N.A.
 RA Wang R.A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Currie J.,
 RA Collura K.;
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC135157; AAC00689.1; --

DR Gramene; Q8GZV6; --
 DR InterPro; IPR001810; F-box.
 DR InterPro; IPR001092; HLH_Basic.
 DR InterPro; IPR002029; Pept_S8_S53.
 DR InterPro; IPR008945; Skp1_Skp2.
 DR InterPro; IPR00626; Ubiquitin.
 DR Pfam; PF00646; F-box; 1.
 DR Pfam; PF00010; HLH; 1.
 DR SMART; SM00256; FBOX; 1.
 DR SMART; SM00353; HLH; 1.
 DR SMART; SM00213; UBO; 1.
 DR PROSITE; PS50181; FBOX; 1.
 DR PROSITE; PS50888; HLH; 1.
 DR PROSITE; PS00136; SUBTILASE_ASP; UNKNOWN_1.
 DR PROSITE; PS50053; UBQUITIN_2; 1.
 DR Hypothetical protein.
 KM SEQUENCE 776 AA; 83902 MW; F05B3429D2B924BD CRC64;

Query Match 7.4%; Score 205; DB 2; Length 776;
 Best Local Similarity 22.0%; Pred. No. 4,5e-05;
 Matches 115; Conservative 90; Mismatches 197; Indels 120; Gaps 25;

QY 1 MRLRLRLKLR-----TWPLEVPEPFLTGLRSHRLSLCTGWSNTRFTTLN 51
 Db 1 MRLRLRLKLR-----TWPLEVPEPFLTGLRSHRLSLCTGWSNTRFTTLN 58
 QY 52 YKDP-LTGD-EETLASVGVSGDLICLLDDIPAPNIPSTDESHSLQNN--EQPSL 106
 Db 52 YKDP-LTGD-EETLASVGVSGDLICLLDDIPAPNIPSTDESHSLQNN--EQPSL 106
 QY 59 RSEHLITDPKATILPALGLASGDLITLTL-SPLSPSPPPQPPQAPLPENPVDVPSI 117
 Db 59 RSEHLITDPKATILPALGLASGDLITLTL-SPLSPSPPPQPPQAPLPENPVDVPSI 117
 QY 107 ATSSNQTSMDQPSDSFOGAASG---VWNDSSMLGPSQNFASISIDNAMAAGTG 162
 Db 107 ATSSNQTSMDQPSDSFOGAASG---VWNDSSMLGPSQNFASISIDNAMAAGTG 162
 QY 118 AGAAPPTKSPVESGSSSMPQALCTNPGLPVASDPHPHP-----DVVMAAFA 166
 Db 118 AGAAPPTKSPVESGSSSMPQALCTNPGLPVASDPHPHP-----DVVMAAFA 166
 QY 163 FYPSPEMLCSVSVEQVPHSLLELYQSAD-----CSDANDALIVLIHLMLESGYI 218
 Db 163 FYPSPEMLCSVSVEQVPHSLLELYQSAD-----CSDANDALIVLIHLMLESGYI 218
 QY 167 VIKSR-----SLVVDVTREKEMNV-GCHDGTVIC-----RLVVALHAILDAGLIVANPV 216
 Db 167 VIKSR-----SLVVDVTREKEMNV-GCHDGTVIC-----RLVVALHAILDAGLIVANPV 216
 QY 219 AKALSMPEKMKLSGVY---KLQYMHF-----LCEGSSATLTCPVLGNLIVNATLKI 267
 Db 219 AKALSMPEKMKLSGVY---KLQYMHF-----LCEGSSATLTCPVLGNLIVNATLKI 267
 QY 217 GSCGLDPQNM-ASGSFVPMKYTLPELVEALPVVEGMAVAVLVSLNGNPMAYG--HV 273
 Db 217 GSCGLDPQNM-ASGSFVPMKYTLPELVEALPVVEGMAVAVLVSLNGNPMAYG--HV 273
 QY 268 NNEISVYRL-----QLLPESFICKKGENVANIYKDLQSLSLFDOCLVYPLATFQ 322
 Db 268 NNEISVYRL-----QLLPESFICKKGENVANIYKDLQSLSLFDOCLVYPLATFQ 322
 QY 274 PGATSGVRLCLPELAPLPLVLDSDVSTABE--REIHELKYLKDEKCLPLMISLQ 330
 Db 274 PGATSGVRLCLPELAPLPLVLDSDVSTABE--REIHELKYLKDEKCLPLMISLQ 330
 QY 323 ALNLPDVGVLVPLLELKLRIPLRLDVASVLSLAVCRDLFTASNDPLMFLYLIRFRD 382
 Db 323 ALNLPDVGVLVPLLELKLRIPLRLDVASVLSLAVCRDLFTASNDPLMFLYLIRFRD 382
 QY 331 LNNLSLPICMALPDPVAKVLEFVPGVDLARVQCTCKELRLADNLVATKKCEMEF-- 386
 Db 331 LNNLSLPICMALPDPVAKVLEFVPGVDLARVQCTCKELRLADNLVATKKCEMEF-- 386

QY 383 NTVRVQDT---DWKELY--RK-----RH10RKESPPKGRFVML----- 415
 Db 389 NT---QDTGCMWCKCIYSDOKRDIYIADKYTCGNVQKPPVQGRMLITLVHSLLCQY 445
 QY 416 -----PSTHTLPFYENPLPFRFPSS 437
 Db 446 ITTGLSLMTHLVLDLVQDAPAGIHFDCITLPIPNPQLPSS 487

RESULT 9

Q9ZUB9 PRELIMINARY; PRT; 350 AA.

AC Q9ZUB9; 01-MAY-1999 (Tremblrel. 10, Created)
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DE F508.32 protein.
 GN Name=F508.32;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 CC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 NCBI_TaxID=3702;

RP SEQUENCE FROM N.A.
 RA Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Liu S., Lenz C.,
 RA Li J., Kremesetskaia I., Luros J., Altafi H., Gonzalez A., Araujo R.,
 RA Buehler E., Conn L., Conway A.B., Dunn P., Hansen N., Hutzar L.,
 RA Kim C., Palm C.J., Rowley D., Shinn P., Walker M., Davis R.W.,
 RA Ecker J.R., Federspiel N.A., Theologis A.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [1]

RP SEQUENCE FROM N.A.
 RA Theologis;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC005990; AAC98032.1; --
 DR PIR; H86371; H86371.
 DR InterPro; IPR001810; F-box.
 DR InterPro; IPR008945; Skp1_Skp2.
 DR Pfam; PF00646; F-box; 1.
 DR SMART; SM00256; FBOX; 1.
 DR PROSITE; PS50181; FBOX; 1.
 DR PROSITE; PS50888; HLH; 1.
 KM SEQUENCE 350 AA; 39953 MW; CD0B4C6791674D6 CRC64;

Query Match 6.8%; Score 187.5; DB 2; Length 350;
 Best Local Similarity 24.4%; Pred. No. 0.00022;
 Matches 90; Conservative 58; Mismatches 118; Indels 103; Gaps 17;

QY 172 SESVSGQVPHSLF-----TLVYSAQCSANDALIVLIHLMLESGYI 213
 Db 22 NSGIEGVPYMDVELAAKSKRLSEPFELKNVLEKSGDTSILT-ALASVHAVMLESGFV 80
 QY 214 --PGTE-----AKALSMPEKMKLSGVYKLCYMHPLCEGSSATLTCPVLGNLIVNATL 265
 Db 81 LDRSGDSKSPKSLLSVSKRTLPBELITRKQNTNV---EAVTVAFQVIGRLVAVYGTIG 137
 QY 266 ---KINNEIRSVKRLQLLPESFICKEL---GENVANIYKDLQSLSLFDOCLVYPLA 318
 Db 136 GSKCRVH--MTSLDKSRFLPVLDLVDTLKEKQSSSYREVFMLMWDVDELVPL- 194
 QY 319 FTRQALNLPDVG-----LVVLPLELKLRIPLRLDVASVLSLAVCRDLFTASNDPLM 372
 Db 195 -----IGLCKKAGLSPCLMLPLTELKLTIELLPVSGISGMACVCTEMRYLADNDLM 249
 QY 373 RFLYLRDFRDNTVAVQ--DTEWKELY-----RKR--HIQRKESPKGRFVMLPSSTHTIP 423
 Db 250 EHKCLEEGKGLMKLYTGDVWKAKFASFWRKRLDLARNPPIKK----- 296
 QY 424 FIPNPLHPPFPSSRLPPIIGBYDQRPITLPIYVQDPISLSLIPGGEIPSPQPPPL----- 478
 Db 297 --SNRFPPLLPDDR-----DREPFDRFG-----PSDFYRFGRLDP 331

QY 479 RPRDPVGP 487
 Db 332 RDRFGPRDP 340

RESULT 10
 PSFL DROME STANDARD; PRT; 270 AA.
 ID PSFL DROME STANDARD; PRT; 270 AA.
 AC Q9Y637;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Putative proteasome inhibitor.
 GN ORFNames=CG8979;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 NC NCBI_TaxID=7227;
 CX [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=Berkely;
 RC MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
 RA Ballew R.M., Basu P.V., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.V., Berens P.V., Bernan B.P., Bhandari D., Bolintsov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brockstein P., Brotler P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Palacios B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup I.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glocker A., Gong F., Gottrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hestlin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lascko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mikhlov G., Milshina N.V., Mobarry C., Morris J., Moshireff A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M.C., Skupski M.P., Smith T.,
 RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhang L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkely; TISSUE=Head;
 RX MEDLINE=2426066; PubMed=12537569;
 RA Stapleton M., Carlson J.W., Brockstein P., Yu C., Champe M.,
 RA George R.A., Guerin H., Krommiller B., Pacle J.M., Park S., Wan K.H.,
 RA Rubin G.M., Celiker S.E.;
 RT "A Drosophila full-length cDNA resource";
 RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
 CC -1- FUNCTION: Could play an important role in control of proteasome
 CC function. Inhibits the hydrolysis of protein and peptide
 CC substrates by the 20S proteasome (by similarity).

CC -1- SIMILARITY: Belongs to the proteasome inhibitor p131 family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@sib-sib.ch).
 CC
 CC EMBL; AE003824; AAM68701.1; -
 CC EMBL; AY058250; AAL13479.1; -
 CC Inctact; Q9Y637; -
 CC DR Flybase; FBgn003669; CG8979.
 CC KW Hypothetical protein; Proteasome.
 CC DOMAIN 169
 CC SEQUENCE 270 AA; 3008 MW; F7972E7634B90555 CRC64;
 SQ
 Query Match 5.3%; Score 147; DB 1; Length 270;
 Best Local Similarity 21.4%; Pred. No. 0.077;
 Matches 83; Conservative 43; Mismatches 90; Indels 172; Gaps 21;
 QY 172 SSSVGGQVPHSLHTYQGS-ADCSNADALVLIHLML-----ESGYIP-QG 216
 Db 5 STAKTGDFPQWDLTKYTKVADVSKSDLLALVHFLTKHYNFRGVGADKTLPEEG 64
 QY 217 TEAKALSPPEKVKLSGV-YKLQYMP-----LCBSSATLTCVPLGNLIVNATLK 266
 Db 65 SLL-----LPDSNDDDTXSLRYVADKMLYLLGHITGSL-----LIMLDLN-TRK 112
 QY 267 INNEFRSVKRLQPLPESFCIKKLGENTANYKIQKLSLFRQOLVPLLA-----FTR 321
 Db 113 VSN-----ICVEETLVPEVKGQ-ITTIMPSASEIVSRRLDVPFTGNSREYTT 163
 QY 322 QALNLPDVGGLVLDLELKLRTFRLLDVRSVLSLSAVCRDFTSNPDLNRFVLRFR 381
 Db 164 QTTNPPRIG-----SDPDL----- 179
 QY 382 DNTVAVQDTMKELVKRKHIOKESPK--GRFVMLPSTHTTIPYPNLPFRPPSSRL 439
 Db 180 -----RIGPRRGSEFI-----PSAFPRPGF--- 202
 QY 440 PGGIIGCEYD-----QRPLTPVQDPISLIGPGETSQQPPLPRPPVPL 488
 Db 203 -PDVVRGGLDPLGRGCHNLFSFPRFMWG-----FGP-----VRRDPFNPPL 244
 QY 489 PGPNDLPGRGQGNDRFPFRPSRGHPTD 516
 Db 245 ---NNRRGQGGIN-----PDHMRPPD 263

RESULT 11
 Q9Y593 PRELIMINARY; PRT; 434 AA.
 ID Q9Y593
 AC Q9Y593;
 DT 01-NOV-1999 (TREMELREL. 12, Created)
 DT 01-NOV-1999 (TREMELREL. 12, Last sequence update)
 DT 01-MAR-2004 (TREMELREL. 26, Last annotation update)
 DE NY-REN-57 antigen (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=99438124; PubMed=10508479;
 RA Scandeneel V., Gure A.O., Jager D., Jager E., Knuth A., Chen Y.-T.,
 RA Old L.J.;
 RT "Antigens recognized by autologous antibody in patients with renal-
 RT cell carcinoma";
 RL Int. J.Cancer 83:456-464(1999).
 DR EMBL; AF15114; AAD42880.1; -

DR InterPro; IPR001810; F-box.
 DR InterPro; IPR005941; 1PR-like.
 DR Pfam; PF00646; F-box; 1.
 DR PROSITE; PS50181; FBOX; 1.
 FT NON TER
 SQ SEQUENCE 434 AA; 48863 MM; CFA074E8371120D CRC64;

Query Match 5.3%; Score 145.5; DB 2; Length 434;
 Best Local Similarity 21.7%; Pred. No. 0.19; Indels 169; Gaps 24;
 Matches 98; Conservative 61; Mismatches 123; Indels 169; Gaps 24;

QY 105 SIATSSNQTSMODEPSPDSFGQAAGVWVNDSDMLG-PSQNFPAESIQDNAMAEGTGF 163
 DB 75 SSAETGRSRHPDQHPSS--GRCRGTESSPSAAGRPA5MAEAE--EDCH----- 122
 QY 164 YPSEPMLCSESYEGVPHSLFTLYQSADCSANDALIVLHLMLESGYIPQGTAKA-L 222
 DB 123 -----SDTVR-----ADDEENSS-----PAETDLOAQL 146
 QY 223 SMPEKWLKSGYKQYMHPLCEG--SSATLTTCVPL-----GNLIYVNTLKINNE----- 270
 DB 147 QM-----FRQWMEFLAPGVSSSNLENRPGRARGLQKTSADTKGQOAKEKA 197
 QY 271 ---IRSV-----KRIQLPE---SFICEKLGENVANYI---KDLQ 302
 DB 198 RELFLKAVEEONGALYEAIKFYRRAMQVLDIEFKITTYRSPDGDGVSNIEDNDD 257
 QY 303 KLSRL---FKDQVYPLLAFTROALNT--PDV---FGVLVPLELKIIRFL-----LD 348
 DB 258 KQADLLSYFQOQ-----LTFQESVYKLCQPELESQIHISVLPMEVLYIFRWVSSDLD 312
 QY 349 VRSVLSIAVGRDLFTASNDPLRFLYLRDFRDNVYR-VQDTWKELYRKRIHQKESP 407
 DB 313 LRLSEQLSLVCGFYICARDEPIWRLACLKVGWGSCTKLVPYTSWREMFLEP-----P 365
 QY 408 KGRFVMLPSSST-----HTIPFPNPLHPRPPSSRLPPGIIGGEYDQ 450
 DB 366 RVRFQGVYISKTYTIRQEGSLDGFYRAMHGVETV---RYIRFPDGHV----- 411
 QY 451 RPTLPYVGDPISSLIPGGETPSOPPLRPR 481
 DB 412 -----MLTTEEPQSIIVPRLTR 430

RESULT 12

Q9NT57 PRELIMINARY; PRT; 547 AA.
 AC Q9NT57;
 ID Q9NT57;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DE Hypothetical protein DKFZp43C0118 (Fragment).
 GN Name=DKFZp43C0118;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Outenwaelder B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann S.;
 RL Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AL137520; CAB70786.1; -
 DR PIR; T46366; T46366;
 DR InterPro; IPR001810; F-box.
 DR InterPro; IPR008941; 1PR-like.
 DR Pfam; PF00646; F-box; 1.
 DR PROSITE; PS50181; FBOX; 1.
 KW Hypothetical protein.
 FT NON TER
 SQ SEQUENCE 547 AA; 62217 MM; A726E815A82DF31 CRC64;

Query Match 5.3%; Score 145.5; DB 2; Length 547;

Best Local Similarity 21.7%; Pred. No. 0.26;
 Matches 98; Conservative 61; Mismatches 123; Indels 169; Gaps 24;

QY 105 SIATSSNQTSMODEPSPDSFGQAAGVWVNDSDMLG-PSQNFPAESIQDNAMAEGTGF 163
 DB 72 SSAETGRSRHPDQHPSS--GRCRGTESSPSAAGRPA5MAEAE--EDCH----- 119
 QY 164 YPSEPMLCSESYEGVPHSLFTLYQSADCSANDALIVLHLMLESGYIPQGTAKA-L 222
 DB 120 -----SDTVR-----ADDEENSS-----PAETDLOAQL 143
 QY 223 SMPEKWLKSGYKQYMHPLCEG--SSATLTTCVPL-----GNLIYVNTLKINNE----- 270
 DB 144 QM-----FRQWMEFLAPGVSSSNLENRPGRARGLQKTSADTKGQOAKEKA 194
 QY 271 ---IRSV-----KRIQLPE---SFICEKLGENVANYI---KDLQ 302
 DB 195 RELFLKAVEEONGALYEAIKFYRRAMQVLDIEFKITTYRSPDGDGVSNIEDNDD 254
 QY 303 KLSRL---FKDQVYPLLAFTROALNT--PDV---FGVLVPLELKIIRFL-----LD 348
 DB 255 KQADLLSYFQOQ-----LTFQESVYKLCQPELESQIHISVLPMEVLYIFRWVSSDLD 309
 QY 349 VRSVLSIAVGRDLFTASNDPLRFLYLRDFRDNVYR-VQDTWKELYRKRIHQKESP 407
 DB 310 LRLSEQLSLVCGFYICARDEPIWRLACLKVGWGSCTKLVPYTSWREMFLEP-----P 362
 QY 408 KGRFVMLPSSST-----HTIPFPNPLHPRPPSSRLPPGIIGGEYDQ 450
 DB 363 RVRFQGVYISKTYTIRQEGSLDGFYRAMHGVETV---RYIRFPDGHV----- 408
 QY 451 RPTLPYVGDPISSLIPGGETPSOPPLRPR 481
 DB 409 -----MLTTEEPQSIIVPRLTR 427

RESULT 13

Q6PKH7 PRELIMINARY; PRT; 403 AA.
 ID Q6PKH7;
 AC Q6PKH7;
 DT 05-JUL-2004 (Tremblrel. 27, Created)
 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
 DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
 DE FBXO9 protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares N.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Cantinici P., Prange C.,
 RA Rana S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McGwan P.J., McKernan K.O., Malek U.A., Gamaralle P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
 RA Vallalao D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
 RA Krzywinski M.I., Skalski U., Small D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]

RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RA Strausberg R.;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC000650; AA00650.2; -
 DR InterPro; IPR001810; F-box.
 DR InterPro; IPR008941; TPR-like.
 DR Pfam; PF00646; F-box; 1.
 DR PROSITE; PSS0181; FBOX; 1.
 SQ SEQUENCE 403 AA; 47361 MW; 1AAALF46C31315SB CRC64;

Query Match 5.2%; Score 144; DB 2; Length 403;
 Best Local Similarity 23.1%; Pred. No. 0.21;
 Matches 74; Conservative 47; Mismatches 90; Indels 110; Gaps 16;

QY 233 VYKIQVHPLCEG--SSATLTCPVPL-----GNLIVNATLKINNE-----IRSV-- 274
 DB 1 MFRQWMEFLAPGVSSNLENRPPCARAGSLQKTSADTKGQOAKERKARELFLKAVEE 60
 QY 275 -----KRLQLPE-----SFICKKLGENVANIY-----KDLOKLSRL--FK 309
 DB 61 EONGALYEAIKFYRAAQVLPDIEFKITTRSPDGGVGNSTYEDNDSDKADLSYFQ 120
 QY 310 DQLYVPLAFTROALN--PDV---FGLVYVPLELKLRIPL-----LDVRSVLSLAV 358
 DB 121 QQ-----LTFQESVYKLCQPELESQIHISVLEMEVLMYIFRWVWSSDLDRLSLEQSLIV 175
 QY 359 CRDLFTASNDPLMFLYLRDPFRONTVR--VQDTMKELRYKRHIQRKSPKGFVWLPS 417
 DB 176 CREGYICARDEIMWRLACLKWGRSCIKLVPTYSKREFLER-----PVRFPDGVYIS 228
 QY 418 ST-----HTIPFPNPLHPRFPSSRLPGIIGGEYDQRPPLPYVGD 460
 DB 229 KTTYIROGEGSLDGFYRAMHQVEY--RYIRFPDGHV----- 264
 QY 461 ISSLIPGGETPSPQFPPLRPR 481
 DB 265 --XMLTPEEPOSTIVPRLRTR 283

RESULT 14
 AA00650 PRELIMINARY; PRT; 403 AA.
 AC AA00650;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE FBXO9 protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primata; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RX MEDLINE=22368257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshyuki S., Canninci P., Prange C.J.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mulvey S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Woley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
 RA Vallatton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buttefield Y.S.,
 RA Krzyzanski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RA Strausberg R.;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC000650; AA00650.2; -
 SQ SEQUENCE 403 AA; 47361 MW; 1AAALF46C31315SB CRC64;

Query Match 5.2%; Score 144; DB 2; Length 403;
 Best Local Similarity 23.1%; Pred. No. 0.21;
 Matches 74; Conservative 47; Mismatches 90; Indels 110; Gaps 16;

QY 233 VYKIQVHPLCEG--SSATLTCPVPL-----GNLIVNATLKINNE-----IRSV-- 274
 DB 1 MFRQWMEFLAPGVSSNLENRPPCARAGSLQKTSADTKGQOAKERKARELFLKAVEE 60
 QY 275 -----KRLQLPE-----SFICKKLGENVANIY-----KDLOKLSRL--FK 309
 DB 61 EONGALYEAIKFYRAAQVLPDIEFKITTRSPDGGVGNSTYEDNDSDKADLSYFQ 120
 QY 310 DQLYVPLAFTROALN--PDV---FGLVYVPLELKLRIPL-----LDVRSVLSLAV 358
 DB 121 QQ-----LTFQESVYKLCQPELESQIHISVLEMEVLMYIFRWVWSSDLDRLSLEQSLIV 175
 QY 359 CRDLFTASNDPLMFLYLRDPFRONTVR--VQDTMKELRYKRHIQRKSPKGFVWLPS 417
 DB 176 CREGYICARDEIMWRLACLKWGRSCIKLVPTYSKREFLER-----PVRFPDGVYIS 228
 QY 418 ST-----HTIPFPNPLHPRFPSSRLPGIIGGEYDQRPPLPYVGD 460
 DB 229 KTTYIROGEGSLDGFYRAMHQVEY--RYIRFPDGHV----- 264
 QY 461 ISSLIPGGETPSPQFPPLRPR 481
 DB 265 --XMLTPEEPOSTIVPRLRTR 283

RESULT 15
 FBX9_HUMAN STANDARD; PRT; 447 AA.
 ID FBX9_HUMAN
 AC Q9UK97; O75986;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 01-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-OCT-2001 (Rel. 45, Last annotation update)
 DE F-box only protein 9.
 GN Name=FBXO9; Synonyms=FBX9;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RX MEDLINE=22935763; PubMed=14574404; DOI=10.1038/nature02055;
 RA Munnell A.J., Palmer S.A., Sims S.K., Edwards C.A., Ashurst J.L.,
 RA Whiting L., Jones M.C., Horton R., Hunt S.E., Scott C.E.,
 RA Gilbert J.G.R., Clamp M.E., Bethel G., Milne S., Ainscough R.,
 RA Almeida J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S.,
 RA Babage A.K., Bagguley C.L., Bailey J., Banerjee R., Barker D.J.,
 RA Barlow K.P., Bates K., Beare D.M., Beasley H., Beasley O., Bird C.P.,
 RA Blakey S.E., Bray-Allen S., Brook J., Brown A.J., Brown J.Y.,
 RA Bluford D.C., Burrill W., Burton J., Carder C., Carter N.P.,
 RA Chapman J.C., Clark S.Y., Clark G., Clee C.M., Clegg S., Copley V.,
 RA Collier R.E., Collins J.E., Colman L.K., Corby N.R., Coville G.J.,
 RA Culley K.M., Dhami P., Davies J., Dunn M., Earthrowl M.E.,

```

Db      105  EONGALVYEAIKRYRRAMOLVDPBIEKRIYVTSRDPGGDGSYINDDDSDSMADLSYFQ 154
QY      310  DOLVVEYLAFTQGANL-----PDV-----FGLVVLPELEKRIERL-----LDRSVLSISAV 358
          165  QC-----LTFQSVYKLOQPELESQIHISVLPHEVLMYIRWVYSSDDLDRISLQSLV 219
QY      359  CRDLFTASNDPLMEFLVYRDFRONTVR-VODTWKELYRRKHIORESEPKGRVMLIPS 417
          Db      220  CRGFYICADPFIWTEIACIKWGRSCIKLVYTSRREMFIER-----PRVRDGYIS 272
QY      418  ST-----HTTPFNPDLHPRPSSSLPGLIGEXYDQRPVYVGD 460
          Db      273  KTTYINGEQSLDGYRRAMQVEY---RYIRFPFDGHV----- 308
QY      461  ISSLIIPGGETSPSQEPLPLPR 481
          Db      309  -MMLTTPPEPOSIVPLRLR 327

Search completed: November 16, 2004, 07:12:30
Job time : 206 secs

```

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OM protein - protein search, using sw model

Run on: November 16, 2004, 06:55:18 ; Search time 154 Seconds
(without alignments)
1215.953 Million cell updates/sec

Title: US-09-927-458-2
Perfect score: 2754
Sequence: 1 MRLRVRLKRTWPLEVEFETE.....DRPPFRPSRGRPTGRLSFM 522

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A_genesecp_23Sep04:*
- 1: genesecp1980s:*
 - 2: genesecp1990s:*
 - 3: genesecp2000s:*
 - 4: genesecp2001s:*
 - 5: genesecp2002s:*
 - 6: genesecp2003as:*
 - 7: genesecp2003bs:*
 - 8: genesecp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2748	99.8	522	6	ADAs7283 Human sec
2	2748	99.8	522	6	ADAs7283 Human sec
3	2748	99.8	522	6	ADAs7283 Human sec
4	2748	99.8	522	6	ADAs7283 Human sec
5	2748	99.8	522	6	ADAs7283 Human sec
6	2748	99.8	522	6	ADAs7283 Human sec
7	2748	99.8	522	6	ADAs7283 Human sec
8	2748	99.8	522	6	ADAs7283 Human sec
9	2748	99.8	522	6	ADAs7283 Human sec
10	2748	99.8	522	6	ADAs7283 Human sec
11	2748	99.8	522	6	ADAs7283 Human sec
12	2748	99.8	522	6	ADAs7283 Human sec
13	2748	99.8	522	6	ADAs7283 Human sec
14	2748	99.8	522	6	ADAs7283 Human sec
15	2748	99.8	522	6	ADAs7283 Human sec
16	2748	99.8	522	6	ADAs7283 Human sec
17	2748	99.8	522	6	ADAs7283 Human sec
18	2748	99.8	522	6	ADAs7283 Human sec
19	2748	99.8	522	6	ADAs7283 Human sec
20	2748	99.8	522	6	ADAs7283 Human sec
21	2748	99.8	522	6	ADAs7283 Human sec
22	2748	99.8	522	6	ADAs7283 Human sec
23	2748	99.8	522	6	ADAs7283 Human sec
24	2748	99.8	522	6	ADAs7283 Human sec
25	2748	99.8	522	6	ADAs7283 Human sec

26	396	14.4	76	8	ABO54274	ABO54274 Human gen
27	299	10.9	113	3	AAy87356	AAy87356 Human sig
28	265.5	9.6	225	4	ABG06838	ABG06838 Novel hum
29	264.5	9.6	53	4	ABG18509	ABG18509 Novel hum
30	264.5	9.6	53	4	ABG18509	ABG18509 Novel hum
31	249	9.0	47	8	ABG32108	ABG32108 Novel hum
32	240.5	8.7	475	3	AAg29404	AAg29404 Arabidops
33	194	7.0	39	3	AAy83054	AAy83054 F-box mot
34	194	7.0	39	5	AAO22459	AAO22459 Human F-b
35	189	6.9	38	2	AAy02272	AAy02272 A F-box p
36	189	6.9	38	4	AAE08044	AAE08044 Human F-b
37	189	6.9	38	7	AAE39652	AAE39652 Human F-b
38	164	6.0	38	2	AAy02273	AAy02273 A F-box p
39	164	6.0	38	4	AAE08045	AAE08045 Mouse F-b
40	164	6.0	38	7	AAE39653	AAE39653 Mouse F-b
41	152.5	5.5	336	3	AAg29406	AAg29406 Arabidops
42	152.5	5.5	342	3	AAg29405	AAg29405 Arabidops
43	147	5.3	270	4	ABG64135	ABG64135 Drosophil
44	145.5	5.3	430	4	AAy41539	AAy41539 Human pol
45	144	5.2	321	3	AAy92341	AAy92341 Human can

ALIGNMENTS

RESULT 1	ADAs7283	ADAs7283 standard; protein; 522 AA.
XX	ADAs7283;	
AC	ADAs7283;	
DT	20-NOV-2003 (first entry)	
XX		
XX	Human secreted protein #566.	
DE		
XX	Immunosuppressive; antiinflammatory; antiasthmatic; anti allergic;	
KW	Cytostatic; cerebroprotective; neuroprotective; neurotropic;	
KW	cardiovascular; antihypertensive; gene therapy;	
KW	human secreted protein; immune disorder; inflammation;	
KW	respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;	
KW	inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;	
KW	multiple sclerosis; ischaemic brain injury; Parkinson's disease;	
KW	Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;	
XX	triple helix formation; antisense gene therapy; forensic biology.	
OS	Homo sapiens.	
XX		
PN	WO2002102994-A2.	
XX		
XX	27-DEC-2002.	
XX		
PF	19-MAR-2002; 2002MO-US008278.	
XX		
PR	21-MAR-2001; 2001US-0277340P.	
PR	19-JUL-2001; 2001US-0306171P.	
PR	13-NOV-2001; 2001US-0331287P.	
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
XX		
PI	Rosen CA, Ruben SM;	
XX		
DR	WPI; 2003-167512/16.	
DR	N-PSDB; ADAs6387.	
XX		
PT	New human secreted polypeptides and polynucleotides, useful for	
PT	diagnosing, treating or preventing e.g. immune disorders, inflammatory	
PT	conditions, respiratory disorders, cancers, CNS disorders, or	
XX	neurodegenerative disorders.	
PS	Claim 13; SEQ ID NO 1473; 1754dp; English.	
XX		
CC	The invention relates to 592 new human secreted polypeptides useful for	
CC	diagnosing, treating or preventing e.g. immune disorders, inflammatory	

CC conditions, respiratory disorders, cancers, CNS disorders, or
CC neurodegenerative disorders, or polypeptides comprising an amino acid
CC sequence at least 95% identical to the new sequences. The polypeptides,
CC antibodies or antibody fragments that bind to the polypeptides, nucleic
CC acids encoding the polypeptides, agonists or antagonists that binds to
CC the polypeptide, are useful in preparing diagnostic or pharmaceutical
CC compositions for diagnosing, treating or preventing an e.g. immune
CC disorders, inflammatory conditions (e.g. inflammatory bowel disease,
CC nephritis or Crohn's disease), respiratory disorders (e.g. asthma and
CC allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
CC (e.g. multiple sclerosis or ischemic brain injury), neurodegenerative
CC disorders (e.g. Parkinson's disease or Alzheimer's disease), and
CC cardiovascular disorders (e.g. atherosclerosis or myocarditis). The
CC polynucleotides are useful for chromosome identification, chromosome
CC mapping, for controlling gene expression through triple helix formation
CC or antisense DNA or RNA, in gene therapy, for identifying individuals
CC from minute biological samples, in forensic biology, and as hybridization
CC probes. The polypeptides are useful for as molecular weight markers on
CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
CC gels, to raise antibodies, for testing biological activities, and for
CC treating or preventing neural disorders, immune system disorders,
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC renal, proliferative and/or cancerous diseases. This sequence corresponds
CC to one of the polypeptide of the invention. Note: The sequence data for
CC this patent did form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 522 AA;

Query Match 99.8%; Score 2748; DB 6; Length 522;
Best Local Similarity 99.8%; Pred. No. 5.3e-239;
Matches 521; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRLKRLKRTWPEPEPEPTGLHLSHLSTLCTGWSNNRFTITNTYKDLTGD 60
DB 1 MRLKRLKRTWPEPEPEPTGLHLSHLSTLCTGWSNNRFTITNTYKDLTGD 60
QY 61 ETLASVIGSDILICLIQDDIPAPNIPSSSTDSHSSLONNEQSLATSSNQTSMD 120
DB 61 ETLASVIGSDILICLIQDDIPAPNIPSSSTDSHSSLONNEQSLATSSNQTSMD 120
QY 61 ETLASVIGSDILICLIQDDIPAPNIPSSSTDSHSSLONNEQSLATSSNQTSMD 120
DB 61 ETLASVIGSDILICLIQDDIPAPNIPSSSTDSHSSLONNEQSLATSSNQTSMD 120
QY 121 SDSFGQAGAGVWNNDSMLGPSONFEAESIQDNNAHMAEGTFPSPMLCSSEVEG 180
DB 121 SDSFGQAGAGVWNNDSMLGPSONFEAESIQDNNAHMAEGTFPSPMLCSSEVEG 180
QY 121 SDSFGQAGAGVWNNDSMLGPSONFEAESIQDNNAHMAEGTFPSPMLCSSEVEG 180
DB 121 SDSFGQAGAGVWNNDSMLGPSONFEAESIQDNNAHMAEGTFPSPMLCSSEVEG 180
QY 181 HSLFTLYOSADCSANDALIVLHLLMLSGYIPQGTAKALSMPEKMKLSGVYKQYMH 240
DB 181 HSLFTLYOSADCSANDALIVLHLLMLSGYIPQGTAKALSMPEKMKLSGVYKQYMH 240
QY 181 HSLFTLYOSADCSANDALIVLHLLMLSGYIPQGTAKALSMPEKMKLSGVYKQYMH 240
DB 181 HSLFTLYOSADCSANDALIVLHLLMLSGYIPQGTAKALSMPEKMKLSGVYKQYMH 240
QY 241 PLCESSATLTCPVPLGNIVNATLKINNEIRSVKRLQLPESTCEKLGENVANTYKD 300
DB 241 PLCESSATLTCPVPLGNIVNATLKINNEIRSVKRLQLPESTCEKLGENVANTYKD 300
QY 241 PLCESSATLTCPVPLGNIVNATLKINNEIRSVKRLQLPESTCEKLGENVANTYKD 300
DB 241 PLCESSATLTCPVPLGNIVNATLKINNEIRSVKRLQLPESTCEKLGENVANTYKD 300
QY 301 LQKLSRLFKDQLVPLAFTROALNLPVFGIVLPLELKURIFRLADVSVLSAVCR 360
DB 301 LQKLSRLFKDQLVPLAFTROALNLPVFGIVLPLELKURIFRLADVSVLSAVCR 360
QY 301 LQKLSRLFKDQLVPLAFTROALNLPVFGIVLPLELKURIFRLADVSVLSAVCR 360
DB 301 LQKLSRLFKDQLVPLAFTROALNLPVFGIVLPLELKURIFRLADVSVLSAVCR 360
QY 361 DLFTNSNPLIMRFLIYLDPRDNVYRVDDTWKLYKRKHQKESKGFVMLPESTH 420
DB 361 DLFTNSNPLIMRFLIYLDPRDNVYRVDDTWKLYKRKHQKESKGFVMLPESTH 420
QY 421 TIFPVPNLHPRFPSSRLPGIIGGEYDQRTLPYVGDPISSILIPGGTSPQFPPLRP 480
DB 421 TIFPVPNLHPRFPSSRLPGIIGGEYDQRTLPYVGDPISSILIPGGTSPQFPPLRP 480
QY 481 RFDVGLIPGNPILIPGSGNDRPFPSPRGRPTDGLSM 522
DB 481 RFDVGLIPGNPILIPGSGNDRPFPSPRGRPTDGLSM 522

RESULT 2
ADA41163

ID ADA41163 standard; protein; 522 AA.
XX ADA41163;
AC ADA41163;
XX 20-NOV-2003 (first entry)
DT 20-NOV-2003 (first entry)
XX Human secreted protein.
DE Human secreted protein.
XX Human; secreted protein; cancer; hyperproliferative disorder;
KW rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;
KW anaemia; allergic reaction; asthma; cardiovascular disorder;
KW wound healing; cytosolic; immunosuppressive; neurotropic; neuroprotective;
KW antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory;
KW vulnery; cardiac; gene therapy.
XX Homo sapiens.
OS Homo sapiens.
PN MO2002102993-A2.
XX 27-DEC-2002.
PD 27-DEC-2002.
XX 19-MAR-2002; 2002MO-US008123.
PF 19-MAR-2002; 2002MO-US008123.
PR 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX (HUMA-) HUMAN GENOME SCI INC.
PA (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Ruben SM;
PI Rosen CA, Ruben SM;
XX WPI, 2003-175238/17.
DR WPI, 2003-175238/17.
XX New human secreted proteins and nucleic acid molecules, useful for
PT preparing a diagnostic or pharmaceutical composition for diagnosing,
PT preventing or treating cancer or other hyperproliferative disorder,
PT asthma, allergies or AIDS.
XX Claim 1, SEQ ID NO 1545; 3205BP; English.
PS The invention relates to novel genes ADA39629-ADA40565 and proteins
XX ADA40566-ADA41501 for human secreted proteins, useful for preventing,
CC treating or ameliorating medical conditions e.g. by protein or gene
CC therapy. The polypeptides, nucleic acid molecules, antibodies or their
CC fragments, and agonists or antagonists that bind to the polypeptide are
CC useful for preparing a diagnostic or pharmaceutical composition for
CC diagnosing or treating cancer or other hyperproliferative disorder. The
CC polypeptides and nucleic acid molecules are also useful for detecting,
CC preventing, diagnosing, prognosticating, treating or ameliorating cancer
CC or other hyperproliferative disorders including neoplasms, autoimmune
CC disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus
CC erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic
CC anaemia), haematopoietic or haematological disorders (e.g. anaemia,
CC thrombocytopenia), allergic reactions including asthma or eczema,
CC inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory
CC bowel disease or Crohn's disease), neurodegenerative disorders (e.g.
CC Alzheimer's disease or Parkinson's disease), cardiovascular disorders
CC (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,
CC fungal or viral infections including HIV/AIDS), or wound healing and
CC disorders of epithelial cell proliferation. The nucleic acids are also
CC useful for chromosome identification, radiation hybrid mapping or long-
CC range restriction mapping, as molecular weight markers, and as
CC hybridization or diagnostic probes. The polypeptides and antibodies are
CC useful for providing immunological probes for differential identification
CC of the tissues immunohistochemistry assays. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 522 AA;

Query Match 99.8%; Score 2748; DB 6; Length 522;
Best Local Similarity 99.8%; Pred. No. 5.3e-239;

Matches 521; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 1 MRLRVRLKRTWPEVETPTLGHRLSHRLSLCTGWGSSNTRFTITLNYKDLTGE 60
D 1 MRLRVRLKRTWPEVETPTLGHRLSHRLSLCTGWGSSNTRFTITLNYKDLTGE 60
QY 61 ETLASYGIVSGDILICLLIQQDIPAPNIPSSSTDESHSLQNNQPSLATSSNQTSMQDOP 120
D 61 ETLASYGIVSGDILICLLIQQDIPAPNIPSSSTDESHSLQNNQPSLATSSNQTSMQDOP 120
QY 121 SDSFGQAAGSGVWMDSMGSPONFEASIQDNNAHAEGTGFPSBPMCSSEVSGQVP 180
D 121 SDSFGQAAGSGVWMDSMGSPONFEASIQDNNAHAEGTGFPSBPMCSSEVSGQVP 180
QY 181 HSLFTLYQSADCSNDALIVLHILMLSEGYIPOGTEAKALSMPEKMKLSGYVYLQYMH 240
D 181 HSLFTLYQSADCSNDALIVLHILMLSEGYIPOGTEAKALSMPEKMKLSGYVYLQYMH 240
QY 241 PLCEGSSATLTCPVLGNLIVNATLTKINNEIRSVKRLQLPESFTCKEKLGENVANITYKD 300
D 241 PLCEGSSATLTCPVLGNLIVNATLTKINNEIRSVKRLQLPESFTCKEKLGENVANITYKD 300
QY 301 LOKLSRLFKDQVPLAFTRQALNLPDVFGVLVPLTELKRLIFRLLDVRSVLSAVCR 360
D 301 LOKLSRLFKDQVPLAFTRQALNLPDVFGVLVPLTELKRLIFRLLDVRSVLSAVCR 360
QY 361 DLFTASNDPLMRFLYRDFRNTVRVQDTMKELYKRKHIOKESPKGFVWLPSSTH 420
D 361 DLFTASNDPLMRFLYRDFRNTVRVQDTMKELYKRKHIOKESPKGFVWLPSSTH 420
QY 421 TIIFYPNLHRRPPSSRLPPGIIGEDYDQRTLPYVGDLSILIPGGTTPSQFPLRP 480
D 421 TIIFYPNLHRRPPSSRLPPGIIGEDYDQRTLPYVGDLSILIPGGTTPSQFPLRP 480
QY 481 RFDVVGPLPGPNPILPGRGPNDRFPFRPSRGRPTDGLSLFM 522
D 481 RFDVVGPLPGPNPILPGRGPNDRFPFRPSRGRPTDGLSLFM 522
```

RESULT 3

ABR47958 standard; protein; 522 AA.

AC ABR47958;

DT 12-JUN-2003 (first entry)

DE Human secreted protein, SEQ ID 849.

KM Cardiac; antiarrhythmic; antiarteriosclerotic; vasotropic; cyostatic;

KW vulnerability; antiinflammatory; nootropic; neuroprotective;

KX antiparkinsonian; gene therapy; human; cardiovascular disorder.

OS Homo sapiens.

PN WO200295010-A2.

PD 28-NOV-2002.

PF 19-MAR-2002; 2002MO-US009785.

PR 21-MAR-2001; 2001US-027734OP.

PR 19-JUL-2001; 2001US-030617IP.

PR 13-NOV-2001; 2001US-0331287P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Ruben SM;

DR WPI; 2003-129429/12.

PT Novel human secreted proteins, useful for detecting, preventing, diagnosing, prognosticating, treating and/or ameliorating cardiovascular

PT disorders such as arrhythmia.

XX Claim 13; SEQ ID NO 849; 1881pp; English.

XX The present invention relates to novel human secreted proteins (ABR47953-ABR48145) and their coding sequences (ACC50344-ACC50856). The proteins and their coding sequences are useful for the preparation of a diagnostic or pharmaceutical composition for diagnosing or treating a cardiovascular disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary arteriosclerosis and myocardial ischemia), neural disorders, immune system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders, pulmonary disorders, renal disorders, for proliferative disorders and/or cancerous diseases and conditions, for wound healing and epithelial cell proliferation, to treat inflammation or infection, for treating thrombosis and arteriosclerosis, for treating or preventing neural damage which occurs in neuronal disorders or neurodegenerative conditions such as Alzheimer's disease and Parkinson's disease, to enhance bone and periodontal regeneration and aid in tissue transplants or bone grafts, to prevent skin aging or hair loss, to stimulate growth and differentiation of haematopoietic cells and bone marrow cells when used in combination with other cytokines, to maintain organs before transplantation or for supporting cell culture of primary tissues, to increase or decrease differentiation or proliferation of embryonic stem cells, or to modulate mammalian characteristics or metabolism. Note: The sequence data for this patent was published in electronic format and is available from WIP0 at ftp.wipo.int/pub/published_pct_sequences

Sequence 522 AA;

Query Match 99.8%; Score 2748; DB 6; Length 522;

Best Local Similarity 99.8%; Pred. No. 5.3e-239;

Matches 521; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 1 MRLRVRLKRTWPEVETPTLGHRLSHRLSLCTGWGSSNTRFTITLNYKDLTGE 60
D 1 MRLRVRLKRTWPEVETPTLGHRLSHRLSLCTGWGSSNTRFTITLNYKDLTGE 60
QY 61 ETLASYGIVSGDILICLLIQQDIPAPNIPSSSTDESHSLQNNQPSLATSSNQTSMQDOP 120
D 61 ETLASYGIVSGDILICLLIQQDIPAPNIPSSSTDESHSLQNNQPSLATSSNQTSMQDOP 120
QY 121 SDSFGQAAGSGVWMDSMGSPONFEASIQDNNAHAEGTGFPSBPMCSSEVSGQVP 180
D 121 SDSFGQAAGSGVWMDSMGSPONFEASIQDNNAHAEGTGFPSBPMCSSEVSGQVP 180
QY 181 HSLFTLYQSADCSNDALIVLHILMLSEGYIPOGTEAKALSMPEKMKLSGYVYLQYMH 240
D 181 HSLFTLYQSADCSNDALIVLHILMLSEGYIPOGTEAKALSMPEKMKLSGYVYLQYMH 240
QY 241 PLCEGSSATLTCPVLGNLIVNATLTKINNEIRSVKRLQLPESFTCKEKLGENVANITYKD 300
D 241 PLCEGSSATLTCPVLGNLIVNATLTKINNEIRSVKRLQLPESFTCKEKLGENVANITYKD 300
QY 301 LOKLSRLFKDQVPLAFTRQALNLPDVFGVLVPLTELKRLIFRLLDVRSVLSAVCR 360
D 301 LOKLSRLFKDQVPLAFTRQALNLPDVFGVLVPLTELKRLIFRLLDVRSVLSAVCR 360
QY 361 DLFTASNDPLMRFLYRDFRNTVRVQDTMKELYKRKHIOKESPKGFVWLPSSTH 420
D 361 DLFTASNDPLMRFLYRDFRNTVRVQDTMKELYKRKHIOKESPKGFVWLPSSTH 420
QY 421 TIIFYPNLHRRPPSSRLPPGIIGEDYDQRTLPYVGDLSILIPGGTTPSQFPLRP 480
D 421 TIIFYPNLHRRPPSSRLPPGIIGEDYDQRTLPYVGDLSILIPGGTTPSQFPLRP 480
QY 481 RFDVVGPLPGPNPILPGRGPNDRFPFRPSRGRPTDGLSLFM 522
D 481 RFDVVGPLPGPNPILPGRGPNDRFPFRPSRGRPTDGLSLFM 522
```

RESULT 4

ADCT74366

ID ADC74366 standard; protein; 522 AA.
XX
AC ADC74366;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human secreted protein - SEQ ID 999.
XX
KW antihaemic; antirheumatic; antiarthritic; antiinflammatory; antithyroid;
KW antidiabetic; immunosuppressive; dermatological; nephrotoxic;
KW antiparkinsonian; neuroprotective; nootropic; antibacterial; virocidic;
KW fungicide; antiparasitic; antiatherosclerotic; vulnery; cytostatic;
KW haemopoietic; haematologic; anaemia; autoimmune disorder;
KW rheumatoid arthritis; inflammation; Grave's disease; diabetes;
KW systemic lupus erythematosus; glomerulonephritis; neurodegenerative;
KW Parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis;
KW cancer; bacterial; viral; fungal; parasitic infection; gene therapy;
human.
XX
OS Homo sapiens.
XX
PN WO2003038663-A2.
XX
PD 08-MAY-2003.
XX
PF 19-MAR-2002; 2002WO-US0082277.
XX
PR 21-MAR-2001; 2001US-0277340P.
XX
PR 19-JUL-2001; 2001US-0306171P.
XX
PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2003-430516/40.
XX
DR N-PSDB; ADC73751.
XX
PT New human secreted polypeptide for diagnosing, preventing or treating
PT hematopoietic or hematologic disorders (e.g. anemia), autoimmune
PT disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer or
PT atherosclerosis).
XX
PS Claim 16; SEQ ID NO 999; 2272pp; English.
XX
CC The invention relates to a novel human secreted polypeptide comprising a
CC defined sequence given in the specification. The polypeptide, nucleic
CC acid molecule, antibody, agonist or antagonist of the invention may be
CC useful for preparing a composition for diagnosing or treating a
CC haemopoietic or haematologic disorder such as anaemia, autoimmune
CC disorders such as rheumatoid arthritis, inflammation, Grave's disease,
CC diabetes, systemic lupus erythematosus or glomerulonephritis,
CC neurodegenerative disorders including Parkinson's disease and Alzheimer's
CC disease, wounds and hyperproliferative disorders including
CC atherosclerosis or cancer as well as bacterial, viral, fungal or
CC parasitic infections. The polypeptide may also be used during gene
CC therapy procedures and for identifying a binding partner by contacting
CC the polypeptide with a binding partner and determining whether the
CC binding partner increases or decreases the activity of the polypeptide.
CC The current sequence is that of the human secreted protein of the
CC invention.
XX
SQ Sequence 522 AA;
XX
Query Match 99.8%; Score 2748; DB 7; Length 522;
Best Local Similarity 99.8%; Pred. No. 5.3e-239;
Matches 521; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MRLRLKRTMPLEVPETETPLGLRSLRLSLCTGWSNNRFTITLNYKQPLTNGDE 60
DB 1 MRLRLKRTMPLEVPETETPLGLRSLRLSLCTGWSNNRFTITLNYKQPLTNGDE 60
QY 61 ETLASVIGSDLLICLLODDIPAPNIPSSITDSEHSSIQNNNEQPSLATSSNQTSMODEQP 120

DB 61 ETLASVIGSDLLICLLODDIPAPNIPSSITDSEHSSIQNNNEQPSLATSSNQTSMODEQP 120
QY 121 SDSFGQAAGSGVWVNDSDMLGSPQNFSAESIQDNAAHAE3GTGYPSSEPMCCSEVGEQVP 180
DB 121 SDSFGQAAGSGVWVNDSDMLGSPQNFSAESIQDNAAHAE3GTGYPSSEPMCCSEVGEQVP 180
QY 181 HSLFTLYGADCSNDALIVLHILMESGYIQGTAKALSMPEKXKLSGVYKLOYMH 240
DB 181 HSLFTLYGADCSNDALIVLHILMESGYIQGTAKALSMPEKXKLSGVYKLOYMH 240
QY 241 PLCEGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQGLPESFICEKLGENVANYKD 300
DB 241 PLCEGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQGLPESFICEKLGENVANYKD 300
QY 301 LQKSLRTRKQQLVYPLLAFTQALNLPVPGIVLPLELKRIRRLLDVRSVLSAAGR 360
DB 301 LQKSLRTRKQQLVYPLLAFTQALNLPVPGIVLPLELKRIRRLLDVRSVLSAAGR 360
QY 361 DLFASNDPLMLRFYLRDFRDNVTRVODTQMKELYRKSHIQKESPKGRFVMLLPSSSTH 420
DB 361 DLFASNDPLMLRFYLRDFRDNVTRVODTQMKELYRKSHIQKESPKGRFVMLLPSSSTH 420
QY 421 TTPFPNPLHPPFPSSRLPGIIGEDYDQRPILPYVGDPISSLLPGRGETPSQFPPLRP 480
DB 421 TTPFPNPLHPPFPSSRLPGIIGEDYDQRPILPYVGDPISSLLPGRGETPSQFPPLRP 480
QY 481 RPDVPGPLPGPVPILPGRGEPYDRPFPSPGRPTDGRLSFM 522
DB 481 RPDVPGPLPGPVPILPGRGEPYDRPFPSPGRPTDGRLSFM 522
RESULT 5
AAB35161
ID AAB35161 standard; protein; 522 AA.
XX
AC AAB35161;
XX
DT 09-APR-2001 (first entry)
XX
DE Human Skp1-associated F-box protein-1 SAF-1beta SEQ ID NO: 10.
XX
KW Human; protein degradation; siah-mediated degradation protein; SMDP;
KW SCF-complex protein; SCF; siah-1alpha; siah-1 interacting protein; SIP;
KW Skp1-associated F-box protein; SAF-1; SAF-2; SMD; cancer; cell division;
KW Skp1-associated destruction-box protein; inflammatory disease.
XX
OS Homo sapiens.
XX
PN WO200007207-A2.
XX
PD 21-DEC-2000.
XX
PF 09-JUN-2000; 2000WO-US015873.
XX
PR 11-JUN-1999; 99US-00330517.
XX
PA (BURN-) BURNHAM INST.
XX
PI Reed JC, Matsuzawa S;
XX
DR WPI; 2001-071273/08.
XX
DR N-PSDB; AAC67285.
XX
PT Siha Mediated Degradation Protein, useful for drug screening, for
PT therapeutic applications and for functional genomics.
XX
PS Claim 15; Page 107-108; 121pp; English.
XX
CC The present invention provides the protein and coding sequences of
CC several siha-mediated degradation proteins and SCF-complex proteins,
CC which are designated siha-1alpha, siha-1 interacting protein (SIP),
CC encodes two proteins due to alternative splicing (SIP-L and SIP-S), Skp1-

CC associated F-box protein-1alpha and beta and -2 (SAF-1alpha, SAF-1beta
CC and SAF-2) and Skp1-associated destruction-box protein (SD). The
CC proteins and their coding sequences are useful in the diagnosis and
CC treatment of cancers, disorders where too little cell division occurs
CC such as bone marrow aplasias, immunodeficiencies and inflammatory
CC diseases including sepsis, fibrosis, arthritis and graft versus host
CC disease
XX

SO Sequence 522 AA;

Query Match 99.6%; Score 2744; DB 4; Length 522;

Best Local Similarity 99.6%; Pred. No. 1.2e-238;

Matches 520; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MRLRVLKRTWPEVEETPTGHLRSHRLSLCTWGYSSNTRFTITLVKDPITGDE 60
D 1 MRLRVLKRTWPEVEETPTGHLRSHRLSLCTWGYSSNTRFTITLVKDPITGDE 60
QY 61 ETLASVIGSGDILICLLIODDIPAPNIPSSSTSEHSSSLQNNQPSLATSSNQTSMODECP 120
D 61 ETLASVIGSGDILICLLIODDIPAPNIPSSSTSEHSSSLQNNQPSLATSSNQTSMODECP 120
QY 121 SDSFGQAAGSVWVNDMSMLGPSQNFPAESIQDNMAHAEGTGYPSFPMLCSSVSGQVP 180
D 121 SDSFGQAAGSVWVNDMSMLGPSQNFPAESIQDNMAHAEGTGYPSFPMLCSSVSGQVP 180
QY 181 HSLFETLYQASDCSDANDALIVLHLMLESGYIPQTEAKALSMPEKMLSGYKIQYMH 240
D 181 HSLFETLYQASDCSDANDALIVLHLMLESGYIPQTEAKALSMPEKMLSGYKIQYMH 240
QY 241 PLCESSATLTCVPLNSLVNATLKINNEIRSVKRLQLLPESFICKKLGENVANIYKD 300
D 241 PLCESSATLTCVPLNSLVNATLKINNEIRSVKRLQLLPESFICKKLGENVANIYKD 300
QY 301 LQKLSRFLPKQOLVPLLAFTROALNLPDVGVLVPLELKLRIPLLDVRSVLSAVCR 360
D 301 LQKLSRFLPKQOLVPLLAFTROALNLPDVGVLVPLELKLRIPLLDVRSVLSAVCR 360
QY 361 DLFTASNDPLMRELYLRDFRDNTRVQDTWKELVYKRAIQRKESPKGFVMLLPBSTH 420
D 361 DLFTASNDPLMRELYLRDFRDNTRVQDTWKELVYKRAIQRKESPKGFVMLLPBSTH 420
QY 421 TIIPYVPLHRRPPSSRLPPGIIGGEYDQPTLPYVGDPISSLIIRPGSTPQFPPLRP 480
D 421 TIIPYVPLHRRPPSSRLPPGIIGGEYDQPTLPYVGDPISSLIIRPGSTPQFPPLRP 480
QY 481 RFDVGPLPGNPILPGRGPNDRFPPRSRGRPTDRLSPM 522
D 481 RFDVGPLPGNPILPGRGPNDRFPPRSRGRPTDRLSPM 522

```

RESULT 6
AAW68521
ID AAW68521 standard; protein; 591 AA.

XX AAW68521;

DT 25-JAN-1993 (first entry)

XX Human RIP-associated protein.

XX Human; RIP-associated protein; RAP; primer; PCR; amplification; probe;

KM hybridization; death domain; MORT module; ICE-like family protease;

XX kinase; TRAF domain; inflammation; cell death; tumour; HIV; infection.

XX Homo sapiens.

XX MO9841624-A1.

XX 24-SEP-1998.

XX 19-MAR-1998; 98WO-IL000125.

PR 19-MAR-1997; 97IL-00120485.

XX (YEDA) YEDA RES & DEV CO LTD.

XX Wallach D, Kovalenko A;

XX MPI; 1998-531565/45.

DR N-PSDB; AAY57200.

PT DNA encoding RIP-associated protein (RAP) - useful for, e.g. treatment of

PS tumour cells or HIV-infected cells.

XX Claim 10; Fig 2; 65pp; English.

CC This sequence represent part of a human RIP-associated protein (RAP). The
CC coding sequence was isolated from a B-cell library by a yeast 2-hybrid
CC screen using the RIP protein devoid of its "death domain" as a bait. The
CC screen isolated a clone of about 1.9 kb. Primers were generated based on
CC the sequence and used to PCR amplify probes for screening a colon and
CC heart cDNA library. A further 300 bp of sequence was determined, which
CC was added to the 1.9 kb of sequence from the B-cell library. The encoded
CC protein does not contain a "death domain", MORT module, ICE-like family
CC protease domain, kinase domain, nor TRAF domains. RAP was shown to bind
CC only to RIP and not to TRADD, MORT-1, p35-R, p75-R or MACH. The protein
CC can be used to modulate or mediate RIP modulated/mediated intracellular
CC effects on the inflammation, cell death or cell survival pathways in
CC which RIP is involved, e.g. for treating tumour cells or HIV-infected
CC cells
XX

SO Sequence 591 AA;

Query Match 91.1%; Score 2510; DB 2; Length 591;

Best Local Similarity 99.6%; Pred. No. 2.1e-217;

Matches 479; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

```

QY 42 SNTRFTITLVKDPITGDEETLASVIGSGDILICLLIODDIPAPNIPSSSTSEHSSSLQNN 101
D 113 SNTRFTITLVKDPITGDEETLASVIGSGDILICLLIODDIPAPNIPSSSTSEHSSSLQNN 172
QY 102 EOPSLATSSNQTSMODECPSPDSFGQAAGSVWVNDMSMLGPSQNFPAESIQDNMAHAEGT 161
D 173 EQ--LATSSNQTSMODECPSPDSFGQAAGSVWVNDMSMLGPSQNFPAESIQDNMAHAEGT 230
QY 162 GYPSBPMLCSSVSGQVPFHSLETLVQASDCSDANDALIVLHLMLESGYIPQTEAKA 221
D 231 GYPSBPMLCSSVSGQVPFHSLETLVQASDCSDANDALIVLHLMLESGYIPQTEAKA 290
QY 222 LEMPEKMLSGYKIQYMHPLCESSATLTCVPLNSLVNATLKINNEIRSVKRLQLLP 281
D 291 LEMPEKMLSGYKIQYMHPLCESSATLTCVPLNSLVNATLKINNEIRSVKRLQLLP 350
QY 282 ESFICKKLGENVANIYKDLQKLSRFLPKQOLVPLLAFTROALNLPDVGVLVPLELKL 341
D 351 ESFICKKLGENVANIYKDLQKLSRFLPKQOLVPLLAFTROALNLPDVGVLVPLELKL 410
QY 342 RIPLLDVRSVLSAVCRDLFTASNDPLMRELYLRDFRDNTRVQDTWKELVYKRAI 401
D 411 RIPLLDVRSVLSAVCRDLFTASNDPLMRELYLRDFRDNTRVQDTWKELVYKRAI 470
QY 402 QRKESPKGFVMLLPBSTHTIIPYVPLHRRPPSSRLPPGIIGGEYDQPTLPYVGDPI 461
D 471 QRKESPKGFVMLLPBSTHTIIPYVPLHRRPPSSRLPPGIIGGEYDQPTLPYVGDPI 530
QY 462 SSLIPGSTPQFPPLRPDPVGPLPGNPILPGRGPNDRFPPRSRGRPTDRLSPM 521
D 531 SSLIPGSTPQFPPLRPDPVGPLPGNPILPGRGPNDRFPPRSRGRPTDRLSPM 590
QY 522 M 522
D 591 M 591

```

RESULT 7

AAV83047	
ID	AAV83047 standard; protein; 482 AA.
XX	
AC	AAV83047;
XX	
DT	16-AUG-2000 (first entry)
XX	
DE	F-box protein FBP-7.
XX	
XX	F-box protein; FBP; diagnosis; treatment; screening; agonist; antagonist;
KW	proliferative disorder; differentiative disorder; breast cancer;
KM	prostate cancer; ovarian cancer; cancer; small cell lung carcinoma;
XX	immune disorder; cardiovascular disorder; inflammatory disorder; human.
XX	
OS	Homo sapiens.
XX	
FN	WO200012679-A1.
XX	
PD	09-MAR-2000.
XX	
PF	27-AUG-1999; 99WO-US019560.
XX	
PR	28-AUG-1998; 98US-0098355P.
PR	03-FEB-1999; 99US-0118568P.
PR	15-MAR-1999; 99US-0124449P.
XX	
PA	(UYNY) UNIV NEW YORK STATE.
PI	Chieaur DS, Pagano M, Latres E;
XX	
DR	WPI, 2000-256635/22.
DR	N-PSDB; AA293356.
XX	
PT	Novel nucleic acid for screening compounds useful for treating
PT	proliferative and differentiative disorders such as cancer and immune
PI	disorders comprises sequences encoding ubiquitin ligases.
XX	
PS	Claim 10; Fig 10a; 245pp; English.
XX	
CC	Nucleic acids encoding substrate-targeting subunits of ubiquitin ligases
CC	with F-box motifs (F-box proteins) are useful for diagnosis of
CC	proliferative and differentiated related disorders by measuring FBP gene
CC	expression. Cells expressing such proteins or their fragments are useful
CC	for screening compounds. The compounds are agonists or antagonists, which
CC	are useful for treating a proliferative or differentiative disorder in a
CC	mammal such as breast, ovarian and prostate cancer and small cell lung
CC	carcinoma and also major opportunistic infections, immune disorders,
CC	cardiovascular diseases and inflammatory disorders. FBP protein, analogs,
CC	derivatives and their subsequences, anti-FBP antibodies are also useful
CC	in diagnosis of the disorders
XX	
SO	Sequence 482 AA;
XX	
Query Match	90.4%; Score 2489; DB 3; Length 482;
Best Local Similarity	98.1%; Pred. No. 1,2e-215;
Matches	472; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
QY	42 SNTRETTITLNYKDPITGDEETLASYGIVSGDILICILLODDIPAPNIPESDSEHSSLONN 101
DB	2 SNTRETTITLNYKDPITGDEETLASYGIVSGDILICILLODDIPAPNIPESDSEHSSLONN 61
QY	102 EOPSLATSSNORMSDDEQPSDFGQAAOSGYWNDMSLFGSONFEASIDNNAHMAEGT 161
DB	62 EOPSLATSSNOTSIDDEQPSDFGQAAOSGYWNDMSLFGSONFEASIDNNAHMAEGT 121
QY	162 GFYPSEPMLCSESYVEQVPHSLIETLYOGADCGDANDALIVILHILMLBSGYIPOGTAKA 221
DB	162 GFYPSEPMLCSESYVEQVPHSLIETLYOGADCGDANDALIVILHILMLBSGYIPOGTAKA 181
QY	222 LSMPEKMLSGYVKI QYMHPLCEGSSATLTCVPLGNLITVWNAATLKINNEITSVRLQLP 281
DB	182 LSMPEKMLSGYVKI QYMHPLCEGSSATLTCVPLGNLITVWNAATLKINNEITSVRLQLP 241

QY	282	ESFCECKEKGNNANYKLOQLSTLFPDOLVYPIILARQALNPVFGVYVLETKL	341
Db	242	ESFCECKEKGNNANYKLOQLSTLFPDOLVYPIILATROALNPVFGVYVLETKL	301
QY	342	RIFRLDVSYSLSAVCRDLFTANNDLWRFYLNRFRONTYRVQDTMKELYRKSHI	401
QY	402	QRKASEPKGRVWMLPBSTHTTTFYFNPPLHPPFPFSSSLPPEIIGGEVDQRTPLPYVDP1	461
Db	362	QRKSEPKGRVWMLPBSTHTTTFYFNPPLHPPFPFSSSLPPEIIGGEVDQRTPLPYVDP1	421
QY	462	SSLIPGGEFPPSQFPPLRPFDPVAPLPGPNPLPGRCGPNDRPPFPSSGRPTDGRLSF	521
Db	422	SSLIPGGEFPPSQFPPLRPFDPVAPLPGPNPLPGRCGPNDRPPFPSSGRPTDGRLSF	481
QY	522	M 522	
Db	482	M 482	
RESULT 8			
ID	AAO22452	standard, protein, 492 AA.	
XX	AAO22452,		
AC			
XX			
DT	11-OCT-2002	(first entry)	
XX			
DE	Human F-box protein FBP7 SEQ ID No 14.		
XX			
KW	Cytostatic; immunomodulator; cardiant; antiinflammatory; antimicrobial;		
KW	proliferative; differentiative disorder; SKP2; F-box protein; cancer;		
KW	ubiquitin ligase; breast cancer; prostate cancer; ovarian cancer;		
KW	small cell lung carcinoma; immune disorder; parathyroid adenoma; FBP;		
KW	inflammatory disorder; lymphoma; major opportunistic infection;		
KW	certain cardiovascular disease; human.		
XX			
OS	Homo sapiens.		
XX			
PN	MO200255665-A2.		
XX			
PD	18-JUL-2002.		
XX			
PF	07-JAN-2002; 2002MO-US000311.		
XX			
PR	05-JAN-2001; 2001US-0260179P.		
XX			
PA	(UYNV) UNIV NEW YORK STATE.		
XX			
PI	Pagano M;		
XX			
DR	WPI; 2002-599665/64.		
XX			
DR	N-PSDB; AAL41047.		
XX			
PT	Screening compounds for treating proliferative disorders, e.g. breast		
XX	cancer or prostate cancer, injections or immune disorders, comprises		
XX	detecting a change in the activity of Skp2 with either p27 or Cks1.		
XX			
PS	Disclosure; Fig 10; 246pp; English.		
XX			
CC	The invention relates to screening compounds useful for the treatment of		
CC	proliferative or differentiative disorders comprising detecting a change		
CC	in the activity of Skp2 (F-box protein). The method is useful for		
CC	screening compounds for the treatment of proliferative or differentiative		
CC	disorders, particularly cancer. These compounds include small molecules,		
CC	or compounds or derivatives or analogues of the new ubiquitin ligases.		
CC	The compounds are useful for treating diseases such as cancer (e.g.		
CC	breast cancer, prostate cancer or ovarian cancer, lymphoma, small cell		
CC	lung carcinoma or parathyroid adenomas), major opportunistic infections,		
CC	immune disorders, certain cardiovascular diseases or inflammatory		
CC	diseases. This sequence represents an F-box protein (FBP) relating to		
CC	the invention		

XX SQ Sequence 482 AA;
 Query Match 90.4%; Score 2489; DB 5; Length 482;
 Best Local Similarity 98.1%; Pred. No. 1.2e-215;
 Matches 472; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 42 SNTREITLTKYKDPDLEETLASVIGSDILCLIQDDIPAPNIPSSITDSEHSSLONN 101
 CC The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising the
 CC nucleic acids encoding the polypeptides and cells genetically engineered
 CC to express them are also useful for producing the proteins. The proteins
 CC are useful in genetic vaccination, testing and therapy, and can be used
 CC as nutritional supplements. They may be used to increase stem cell
 CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
 CC and/or nerve tissue growth or regeneration; immune suppression and/or
 CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
 CC AAU29510-AAU3304 represent the amino acid sequences of novel human
 CC secreted proteins of the invention

DB 242 ESFICKERKLGNNVNIYKDKLSRLFKDQVLPVLAFTGQALNPVPGVLAFLPLK 301
 QY 282 ESFICKERKLGNNVNIYKDKLSRLFKDQVLPVLAFTGQALNPVPGVLAFLPLK 341
 DB 342 RIFELLDVRSVLSAVCRDLFTASNDPLLMRLYLADFEDNTVRVODTDMKELYKRHI 401
 DB 302 RIFELLDVRSVLSAVCRDLFTASNDPLLMRLYLADFEDNTVRVODTDMKELYKRHI 361

QY 402 CRKSPKGRFVMLLPSSSTHTIPFPNPLHRRPPSSSLPPGIIIGGEVDQPTLPYGDPI 461
 DB 362 CRKSPKGRFVMLLPSSSTHTIPFPNPLHRRPPSSSLPPGIIIGGEVDQPTLPYGDPI 421

QY 462 SSLLPGGETPSQPPPLRPFPDPVGPLPGPNPLPGRGPNDRFPFPPSGRPTDRLSP 521
 DB 422 SSLLPGGETPSQPPPLRPFPDPVGPLPGPNPLPGRGPNDRFPFPPSGRPTDRLSP 481

QY 522 M 522
 DB 482 M 482

RESULT 9
 AAU32109
 ID AAU32109 standard; protein; 607 AA.
 XX AAU32109;
 AC AAU32109;
 DT 18-DEC-2001 (first entry)
 XX DE Novel human secreted protein #2600.
 XX Human; vaccination; gene therapy; nutritional supplement;
 XX stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 XX immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 OS Homo sapiens.
 XX WO200179449-A2.
 PD 25-OCT-2001.
 XX 16-APR-2001; 2001WO-US008656.
 XX 18-APR-2000; 2000US-00552929.
 XX 26-JAN-2001; 2001US-00770160.
 XX (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Drmanac RT;
 XX

DR WPI; 2001-611725/70.
 XX Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy.
 XX Claim 20; Page 556; 765pp; English.
 XX

CC The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising the
 CC nucleic acids encoding the polypeptides and cells genetically engineered
 CC to express them are also useful for producing the proteins. The proteins
 CC are useful in genetic vaccination, testing and therapy, and can be used
 CC as nutritional supplements. They may be used to increase stem cell
 CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
 CC and/or nerve tissue growth or regeneration; immune suppression and/or
 CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
 CC AAU29510-AAU3304 represent the amino acid sequences of novel human
 CC secreted proteins of the invention

XX SQ Sequence 607 AA;
 Query Match 88.9%; Score 2448.5; DB 4; Length 607;
 Best Local Similarity 90.8%; Pred. No. 7.9e-212;
 Matches 481; Conservative 7; Mismatches 33; Indels 9; Gaps 5;

QY 1 MRLRRLKRTPLPELVPEPEPTLGLRSHRLSLCTGYSNTRFTTLNKKDPLTGE 60
 DB 36 MRLRRLKRTPLPELVPEPEPTLGLRSHRLSLCTGYSNTRFTTLNKKDPLTGE 95

QY 61 ETLASVIGSDILCLILQDDIPAPNIPSSITDSEHSSLONNQPSLATSSNOTSQMDQP 120
 DB 96 ETLASVIGSDILCLILQDDIPAPNIPSSITDSEHSSLONNQPSLATSSNOTSQMDQP 155

QY 121 SDSPQQAAGSGVWVNDSDMLGPSQNFEBASIODNAMAEGGFYSEPMLCSESVGQVP 180
 DB 156 SDSPQQAAGSGVWVNDSDMLGPSQNFEBASIODNAMAEGGFYSEPMLCSESVGQVP 215

QY 181 HSLFTLYGADGSDANDALIYLIHILMESGYIPQGTAKALSMPEKRLSGVYLQYMH 240
 DB 216 HSLFTLYGADGSDANDALIYLIHILMESGYIPQGTAKALSMPEKRLSGVYLQYMH 275

QY 241 PLCEGSSATLTCVPLGNLIVNATLKINNEIRSVKQLQLPESPTCKEKGNNVNIYKD 300
 DB 276 PLCEGSSATLTCVPLGNLIVNATLKINNEIRSVKQLQLPESPTCKEKGNNVNIYKD 335

QY 301 LOKLSRLPDDQVLYPLAFTQALNPVPGVLYVLELKRIFELLDVRSVLSAVCR 360
 DB 336 LOKLSRLPDDQVLYPLAFTQALNPVPGVLYVLELKRIFELLDVRSVLSAVCR 395

QY 361 DLFTASNDPLLMRFLYLADFEDNTVRVODTDMKELYRKRHIQKSPKGRFVMLPSSSTH 420
 DB 396 DLFTASNDPLLMRFLYLADFEDNTVRVODTDMKELYRKRHIQKSPKGRFVMLPSSSTH 455

QY 421 TTFPFPNPLHRRPPSSSLPPGIIIGGEVDQPTLPYGDPISSILPFG-GETPS-QPP 477
 DB 456 TTFPFPNPLHRRPPSSSLPPGIIIGGEVDQPTLPYGDPISSILPFG-GETPS-QPP 515

QY 478 -----LRPFPDPVGPLPGPNPLPGRGPNDRFPFPPSGRPTDRLSPF 522
 DB 516 TETHALNPSWPPISSDPNPQSCPGAEGGPPNTRPPPLRPQ-GGRANLM 564

RESULT 10
 ABB90109
 ID ABB90109 standard; protein; 462 AA.
 XX ABB90109;
 AC ABB90109;

XX 24-MAY-2002 (first entry)
 DT Human polypeptide SEQ ID NO 2485.
 XX
 DE
 XX
 KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
 KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;
 KW vulnary; anticarcinogenic; antibacterial; antifungal; antiparasitic;
 KW cardiac; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein.
 XX
 OS Homo sapiens.
 XX
 PN WO200190304-A2.
 XX
 PD 29-NOV-2001.
 XX
 PF 18-MAY-2001; 2001WO-US016450.
 XX
 PR 19-MAY-2000; 2000US-0205515P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Birse CE, Rosen CA;
 XX
 DR WPI; 2002-122018/16.
 DR N-PSDB; ABL90518.
 XX
 PT Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
 PT prevention of neural, immune system, muscular, reproductive,
 PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
 PT disorders.
 XX
 PS Claim 11; SEQ ID NO 2485; 2081bp + Sequence Listing; English.
 XX
 CC The invention relates to novel genes (ABL89449-ABL90553) and proteins
 CC (AB89040-AB89044) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
 CC ovarian cancer; and other cancers of the adrenal gland, bone, bone marrow,
 CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
 CC cardiovascular disorders such as myocardial ischaemia; (d) wound healing
 CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
 CC infectious diseases such as viral, bacterial, fungal and parasitic
 CC infections. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 462 AA;

Query Match 87.3%; Score 2404; DB 5; Length 462;
 Best Local Similarity 88.1%; Pred. No. 5-Se-208;
 Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;
 OY 1 MLRLRLIKRTWPELEPETEPTLGLHSRLSLSLCTWGYSSNRTFTITLYKDPDTGDE 60
 DB 1 MLRLRLIKRTWPELEPETEPTLGLHSRLSLSLCTWGYSSNRTFTITLYKDPDTGDE 60
 OY 61 ETLASVGVSGDLTLIQQDIPAPNIPSSSTDSHSSIQNNEQSLTSSNQMSMOEOP 120
 DB 61 ETLASVGVSGDLTLIQQDIPAPNIPSSSTDSHSSIQNNEQSLTSSNQMSMOEOP 120
 OY 121 SDSFGQAAGQVWMDSLGPSQNFEEASIQDAAHNAEGGFAPSEPMLCSESEVGEQVP 180
 DB 121 SDSFGQAAGQVWMDSLGPSQNFEEASIQDAAHNAEGGFAPSEPMLCSESEVGEQVP 180
 OY 181 HSLFTLYQSADCSANDALIVLHLLMLESGYIQGTBAKALSMPEKXKLSGVYKLOYMH 240
 DB 181 HSLFTLYQSADCSANDALIVLHLLMLESGYIQGTBAKALSMPEKXKLSGVYKLOYMH 240

DB 181 HSLFTLYQSADCSANDALIVLHLLMLESGYIQGTBAKALSMPEKXKLSGVYKLOYMH 240
 OY 241 PLCEGSSATLTCVPLIGNLIVNATLKINNEIRSVKQLLPESFCEKLGNNANITYKD 300
 DB 241 PLCEGSSATLTCVPLIGNLIVN----- 262
 OY 301 LQKRLRFQDQVYVPLAFTROALNLPVFGVIVVPLELKLIRFLLDVRSVLSAVCR 360
 DB 263 -----ANLPDVFGVIVVPLELKLIRFLLDVRSVLSAVCR 300
 OY 361 DLFTASNDPLWRFPLYLDFRDNVTVODTWMKELYRRKHQKESPKGRVWMLPSSTH 420
 DB 301 DLFTASNDPLWRFPLYLDFRDNVTVODTWMKELYRRKHQKESPKGRVWMLPSSTH 360
 OY 421 TTPFYPNLPHPFPSSRLPGIIGGEYDQPTLPYVDDPISLLPGGZTPSQPPPLRP 480
 DB 361 TTPFYPNLPHPFPSSRLPGIIGGEYDQPTLPYVDDPISLLPGGZTPSQPPPLRP 420
 OY 481 RPDVGPPLPGPNILPGRGPNDRPFRPSSRGRPTGRLSPM 522
 DB 421 RPDVGPPLPGPNILPGRGPNDRPFRPSSRGRPTGRLSPM 462
 RESULT 11
 ADA57586
 ID ADA57586 standard; protein; 462 AA.
 XX
 AC ADA57586;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human secreted protein #566.
 XX
 KW Immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;
 KW cytostatic; cerebroprotective; neuroprotective; nootropic;
 KW cardiovascular; antiarteriosclerotic; gene therapy;
 KW human secreted protein; immune disorder; inflammation;
 KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;
 KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;
 KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;
 KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;
 KW triple helix formation; antisense gene therapy; forensic biology.
 XX
 OS Homo sapiens.
 XX
 PN WO2002102994-A2.
 XX
 PD 27-DEC-2002.
 XX
 PF 19-MAR-2002; 2002WO-US008278.
 XX
 PR 21-MAR-2001; 2001US-0277340P.
 PR 19-JUL-2001; 2001US-0306171P.
 PR 13-NOV-2001; 2001US-0331287P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM;
 XX
 DR WPI; 2003-167512/16.
 DR N-PSDB; ADA56693.
 XX
 PT New human secreted polypeptides and polynucleotides, useful for
 PT diagnosing, treating or preventing e.g. immune disorders, inflammatory
 PT conditions, respiratory disorders, cancers, CNS disorders, or
 PT neurodegenerative disorders.
 XX
 PS Claim 13; SEQ ID NO 1779; 1754bp; English.
 XX
 CC The invention relates to 592 new human secreted polypeptides useful for
 CC diagnosing, treating or preventing e.g. immune disorders, inflammatory
 CC conditions, respiratory disorders, cancers, CNS disorders, or
 CC neurodegenerative disorders, or polypeptides comprising an amino acid

sequence at least 95% identical to the new sequences. The polypeptides, antibodies or antibody fragments that bind to the polypeptides, nucleic acids encoding the polypeptides, agonists or antagonists that binds to the polypeptide, are useful in preparing diagnostic or pharmaceutical compositions for diagnosing, treating or preventing an e.g. immune disorders, inflammatory conditions (e.g. inflammatory bowel disease, nephritis or Crohn's disease), respiratory disorders (e.g. asthma and allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative disorders (e.g. Parkinson's disease or Alzheimer's disease), and cardiovascular disorders (e.g. atherosclerosis or myocarditis). The polynucleotides are useful for chromosome identification, chromosome mapping, for controlling gene expression through triple helix formation or antisense DNA or RNA, in gene therapy, for identifying individuals from minute biological samples, in forensic biology, and as hybridization probes. The polypeptides are useful for as molecular weight markers on sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) gels, to raise antibodies, for testing biological activities, and for treating or preventing neural disorders, immune system disorders, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, proliferative and/or cancerous diseases. This sequence corresponds to one of the polypeptide of the invention. Note: The sequence data for this patent did form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 462 AA:

Query Match 87.3%; Score 2404; DB 6; Length 462;

Best Local Similarity 88.1%; Pred. No. 5.5e-208; Mismatches 2; Indels 60; Gaps 1;

Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;

QY 1 MRLNRLLIKRTWPLEVETETETGLHRSRLSLCTWGYSSNTRFTITNXYDPLTGD 60
 Db 1 MRLNRLLIKRTWPLEVETETETGLHRSRLSLCTWGYSSNTRFTITNXYDPLTGD 60
 QY 61 ETLASVGVSGDILCLIQDDIPAPNTPSSDPSHSSLONNEOGLATSSNOMDEOP 120
 Db 61 ETLASVGVSGDILCLIQDDIPAPNTPSSDPSHSSLONNEOGLATSSNOMDEOP 120
 QY 121 SDSFOGAAGSVMNDSDMLGPSQNFPAESIODVNAHAEGTGFPSHPMLCSSEVEGQP 180
 Db 121 SDSFOGAAGSVMNDSDMLGPSQNFPAESIODVNAHAEGTGFPSHPMLCSSEVEGQP 180
 QY 121 SDSFOGAAGSVMNDSDMLGPSQNFPAESIODVNAHAEGTGFPSHPMLCSSEVEGQP 180
 Db 121 SDSFOGAAGSVMNDSDMLGPSQNFPAESIODVNAHAEGTGFPSHPMLCSSEVEGQP 180
 QY 181 HSELTIVQASDCSANDALIVLHLMLESGYIPQGTAKALSMPEKWLKSGYKQYMH 240
 Db 181 HSELTIVQASDCSANDALIVLHLMLESGYIPQGTAKALSMPEKWLKSGYKQYMH 240
 QY 181 HSELTIVQASDCSANDALIVLHLMLESGYIPQGTAKALSMPEKWLKSGYKQYMH 240
 Db 181 HSELTIVQASDCSANDALIVLHLMLESGYIPQGTAKALSMPEKWLKSGYKQYMH 240
 QY 241 PLGCGSATLTCTVPLGNLIVNATLKINNEIRSVKRLPLEPSTCKELGENVANLYKD 300
 Db 241 PLGCGSATLTCTVPLGNLIVNATLKINNEIRSVKRLPLEPSTCKELGENVANLYKD 300
 QY 241 PLGCGSATLTCTVPLGNLIVNATLKINNEIRSVKRLPLEPSTCKELGENVANLYKD 300
 Db 241 PLGCGSATLTCTVPLGNLIVNATLKINNEIRSVKRLPLEPSTCKELGENVANLYKD 300
 QY 301 LQKLSLRFKQOLVPLIAFTROALNPDVGLVVLPELKIRIFRLIDVSVLSAVCR 360
 Db 301 LQKLSLRFKQOLVPLIAFTROALNPDVGLVVLPELKIRIFRLIDVSVLSAVCR 360
 QY 301 LQKLSLRFKQOLVPLIAFTROALNPDVGLVVLPELKIRIFRLIDVSVLSAVCR 360
 Db 301 LQKLSLRFKQOLVPLIAFTROALNPDVGLVVLPELKIRIFRLIDVSVLSAVCR 360
 QY 361 DLFTASNDPLMLRFLYLRDPNDNTVRVODTQWKELYEKRMHQRESKRGFWMLPSSTH 420
 Db 361 DLFTASNDPLMLRFLYLRDPNDNTVRVODTQWKELYEKRMHQRESKRGFWMLPSSTH 420
 QY 421 TIFPYPNPLHRRPPSSRLPPGIIIGGEYDQPTLPYVGDPISSILPPGCTPSQFPPLRP 480
 Db 421 TIFPYPNPLHRRPPSSRLPPGIIIGGEYDQPTLPYVGDPISSILPPGCTPSQFPPLRP 480
 QY 481 RFDVGLPGLPGRNPLIPRGSGNDSPRRPSRGRTDRLSLFM 522
 Db 481 RFDVGLPGLPGRNPLIPRGSGNDSPRRPSRGRTDRLSLFM 522
 QY 481 RFDVGLPGLPGRNPLIPRGSGNDSPRRPSRGRTDRLSLFM 522
 Db 481 RFDVGLPGLPGRNPLIPRGSGNDSPRRPSRGRTDRLSLFM 522
 QY 421 RFDVGLPGLPGRNPLIPRGSGNDSPRRPSRGRTDRLSLFM 462
 Db 421 RFDVGLPGLPGRNPLIPRGSGNDSPRRPSRGRTDRLSLFM 462

RESULT 12
 ADA41482
 ID ADA41482 standard; protein; 462 AA.

AC ADA41482;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human secreted protein.
 XX
 KW Human; secreted protein; cancer; hyperproliferative disorder;
 KW Rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;
 KW Anaemia; allergic reaction; asthma; cardiovascular disorder;
 KW wound healing; cytotoxic; immunosuppressive; nootropic; neuroprotective;
 KW antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory;
 KW vulnerrary; cardiac; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN MO2002102993-A2.
 XX
 PD 27-DEC-2002.
 XX
 PF 19-MAR-2002; 2002WO-US008123.
 XX
 PR 21-MAR-2001; 2001US-0277340P.
 XX
 PR 19-JUL-2001; 2001US-0306171P.
 XX
 PR 13-NOV-2001; 2001US-0331287P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM;
 XX
 DR MPI; 2003-175238/17.
 XX
 PT New human secreted proteins and nucleic acid molecules, useful for
 PT preparing a diagnostic or pharmaceutical composition for diagnosing,
 PT preventing or treating cancer or other hyperproliferative disorder,
 PT asthma, allergies or AIDS.
 XX
 PS Claim 1; SEQ ID NO 1865; 3205bp; English.
 XX
 CC The invention relates to novel genes ADA39629-ADA40565 and proteins
 CC ADA40566-ADA41501 for human secreted proteins, useful for preventing,
 CC treating or ameliorating medical conditions e.g. by protein or gene
 CC therapy. The polypeptides, nucleic acid molecules, antibodies or their
 CC fragments, and agonists or antagonists that bind to the polypeptide are
 CC useful for preparing a diagnostic or pharmaceutical composition for
 CC diagnosing or treating cancer or other hyperproliferative disorder. The
 CC polypeptides and nucleic acid molecules are also useful for detecting,
 CC preventing, diagnosing, prognosticating, treating or ameliorating cancer
 CC or other hyperproliferative disorders including neoplasms, autoimmune
 CC disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus
 CC erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic
 CC anaemia), haematopoietic or haematological disorders (e.g. anaemia,
 CC thrombocytopenia), allergic reactions including asthma or eczema,
 CC inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory
 CC bowel disease or Crohn's disease), neurodegenerative disorders (e.g.
 CC Alzheimer's disease or Parkinson's disease), cardiovascular disorders
 CC (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,
 CC fungal or viral infections including HIV/AIDS), or wound healing and
 CC disorders of epithelial cell proliferation. The nucleic acids are also
 CC useful for chromosome identification, radiation hybrid mapping or long-
 CC range restriction mapping, as molecular weight markers, or as
 CC hybridization or diagnostic probes. The polypeptides and antibodies are
 CC useful for providing immunological probes for differential identification
 CC of the tissues immunohistochemistry assays. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 462 AA;

Query Match 87.3%; Score 2404; DB 6; Length 462;
 Best Local Similarity 88.1%; Pred. No. 5.5e-208;
 Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;

QY 1 MRLRVLLKRTWPLEVPEPETEPTLGLRSHLSLLCTGWGSSNRTFTITLNYKDLPTGDE 60
 DB 1 MRLRVLLKRTWPLEVPEPETEPTLGLRSHLSLLCTGWGSSNRTFTITLNYKDLPTGDE 60
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 DB 61 ETLASVIGSDILICLILODDIPAPNIPSSSTDSHSSLONNQPSLATSSNQTSXQDEOP 120
 QY 121 SDSFGQAAQSGVWVNDMSLGPSONFEAESIODNNAHMAEGTGFYSEPMLCSESVGEQVP 180
 DB 121 SDSFGQAAQSGVWVNDMSLGPSONFEAESIODNNAHMAEGTGFYSEPMLCSESVGEQVP 180
 QY 181 HSELTLYQSADCSNDALIVLIHLLMESGYIPQGTAKALSMPEKMLSGVYKLOVMH 240
 DB 181 HSELTLYQSADCSNDALIVLIHLLMESGYIPQGTAKALSMPEKMLSGVYKLOVMH 240
 QY 241 PLCEGSSATLTGCVPLGNLIVNATLKINNEIRSVRLQLLPESPTCKEKLGENVANITYKD 300
 DB 241 PLCEGSSATLTGCVPLGNLIVN----- 262
 QY 301 LQKLSRLFKDQLVYPLAFTROALNLPVFGVLVPLELKLRIFFLLDVRSVLSAVCR 360
 DB 263 -----ALNLPVFGVLVPLELKLRIFFLLDVRSVLSAVCR 300
 QY 361 DLFTASNDPLLMRFYLRLDFRDNVTRVODTDWKELYRKRHIQRKESKGRFVMLPSSTH 420
 DB 301 DLFTASNDPLLMRFYLRLDFRDNVTRVODTDWKELYRKRHIQRKESKGRFVMLPSSTH 360
 QY 421 TIFPFYNPPLHRRPPSSRLPGIIGGEYDQRTLPYVGDPISSILPGGEMPSQFPPLRP 480
 DB 361 TIFPFYNPPLHRRPPSSRLPGIIGGEYDQRTLPYVGDPISSILPGGEMPSQFPPLRP 420
 QY 481 RFDVPGLPGPNPILPGRGPNDRPFRPSRGRPTDGRLSFM 522
 DB 421 RFDVPGLPGPNPILPGRGPNDRPFRPSRGRPTDGRLSFM 462

RESULT 13
 ID ABR48139 standard; protein; 462 AA.
 AC ABR48139;
 XX
 DT 12-JUN-2003 (first entry)
 XX
 DE Human secreted protein, SEQ ID 1030.
 XX
 KW Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cyostatic;
 KW vulnereary; antiinflammatory; neuroprotective;
 KW antiparkinsonian; gene therapy; human; cardiovascular disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200295010-A2.
 XX
 PD 28-NOV-2002.
 XX
 PF 19-MAR-2002; 2002WO-US009785.
 XX
 PR 21-MAR-2001; 2001US-0277340P.
 PR 19-JUL-2001; 2001US-0306171P.
 PR 13-NOV-2001; 2001US-0331287P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM;
 XX
 DR WPI; 2003-129429/12.
 XX
 PT Novel human secreted proteins, useful for detecting, preventing,
 PT diagnosing, prognosticating, treating and/or ameliorating cardiovascular
 PT disorders such as arrhythmia.

PS Claim 13; SEQ ID NO 1030; 1881bp; English.
 XX
 CC The present invention relates to novel human secreted proteins (ABR47633-
 CC ABR48145) and their coding sequences (ACC050344-ACC050856). The proteins
 CC and their coding sequences are useful for the preparation of a diagnostic
 CC or pharmaceutical composition for diagnosing or treating a cardiovascular
 CC disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary
 CC arteriosclerosis and myocardial ischaemia), neural disorders, immune
 CC system disorders, muscular disorders, reproductive disorders,
 CC gastrointestinal disorders, pulmonary disorders, renal disorders,
 CC proliferative disorders and/or cancerous diseases and conditions, for
 CC wound healing and epithelial cell proliferation, to treat inflammation or
 CC infection, for treating thrombosis and arteriosclerosis, for treating or
 CC preventing neural damage which occurs in neuronal disorders or
 CC neurodegenerative conditions such as Alzheimer's disease and Parkinson's
 CC disease, to enhance bone and periodontal regeneration and aid in tissue
 CC transplants or bone grafts, to prevent skin aging or hair loss, to
 CC stimulate growth and differentiation of haematopoietic cells and bone
 CC marrow cells when used in combination with other cytokines, to maintain
 CC organs before transplantation or for supporting cell culture of primary
 CC tissues, to increase or decrease differentiation or proliferation of
 CC embryonic stem cells, or to modulate mammalian characteristics or
 CC metabolism. Note: The sequence data for this patent was published in
 CC electronic format and is available from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 462 AA;
 Query Match 87.3%; Score 2404; DB 6; Length 462;
 Best Local Similarity 88.1%; Pred. No. 5; se=208;
 Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;

QY 1 MRLRVLLKRTWPLEVPEPETEPTLGLRSHLSLLCTGWGSSNRTFTITLNYKDLPTGDE 60
 DB 1 MRLRVLLKRTWPLEVPEPETEPTLGLRSHLSLLCTGWGSSNRTFTITLNYKDLPTGDE 60
 QY 61 ETLASVIGSDILICLILODDIPAPNIPSSSTDSHSSLONNQPSLATSSNQTSXQDEOP 120
 DB 61 ETLASVIGSDILICLILODDIPAPNIPSSSTDSHSSLONNQPSLATSSNQTSXQDEOP 120
 QY 121 SDSFGQAAQSGVWVNDMSLGPSONFEAESIODNNAHMAEGTGFYSEPMLCSESVGEQVP 180
 DB 121 SDSFGQAAQSGVWVNDMSLGPSONFEAESIODNNAHMAEGTGFYSEPMLCSESVGEQVP 180
 QY 181 HSELTLYQSADCSNDALIVLIHLLMESGYIPQGTAKALSMPEKMLSGVYKLOVMH 240
 DB 181 HSELTLYQSADCSNDALIVLIHLLMESGYIPQGTAKALSMPEKMLSGVYKLOVMH 240
 QY 241 PLCEGSSATLTGCVPLGNLIVNATLKINNEIRSVRLQLLPESPTCKEKLGENVANITYKD 300
 DB 241 PLCEGSSATLTGCVPLGNLIVN----- 262
 QY 301 LQKLSRLFKDQLVYPLAFTROALNLPVFGVLVPLELKLRIFFLLDVRSVLSAVCR 360
 DB 263 -----ALNLPVFGVLVPLELKLRIFFLLDVRSVLSAVCR 300
 QY 361 DLFTASNDPLLMRFYLRLDFRDNVTRVODTDWKELYRKRHIQRKESKGRFVMLPSSTH 420
 DB 301 DLFTASNDPLLMRFYLRLDFRDNVTRVODTDWKELYRKRHIQRKESKGRFVMLPSSTH 360
 QY 421 TIFPFYNPPLHRRPPSSRLPGIIGGEYDQRTLPYVGDPISSILPGGEMPSQFPPLRP 480
 DB 361 TIFPFYNPPLHRRPPSSRLPGIIGGEYDQRTLPYVGDPISSILPGGEMPSQFPPLRP 420
 QY 481 RFDVPGLPGPNPILPGRGPNDRPFRPSRGRPTDGRLSFM 522
 DB 421 RFDVPGLPGPNPILPGRGPNDRPFRPSRGRPTDGRLSFM 462

RESULT 14
 ID ADC74596 standard; protein; 462 AA.
 XX

AC ADC74596;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE Human secreted protein - SEQ ID 1229.
 XX
 KM antiataemic; antirheumatic; antiarthritic; antiinflammatory; antithyroid;
 KM antidiabetic; immunosuppressive; dermatological; nephrotoxic;
 KM antiparkinsonian; neuroprotective; nootropic; antibacterial; virucide;
 KM fungicide; antiparasitic; antiatherosclerotic; vulnerary; cytosstatic;
 KM haemopoietic; haematologic; anaemia; autoimmune disorder;
 KM rheumatoid arthritis; inflammation; Grave's disease; diabetes;
 KM systemic lupus erythematosus; glomerulonephritis; neurodegenerative;
 KM Parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis;
 KM cancer; bacterial; viral; fungal; parasitic infection; gene therapy;
 KM human.
 XX
 OS Homo sapiens.
 XX
 PN WC0003038063-A2.
 XX
 PD 08-MAY-2003.
 XX
 PF 19-MAR-2002; 2002WC-US008277.
 XX
 PR 21-MAR-2001; 2001US-0277340P.
 PR 19-JUN-2001; 2001US-0306171P.
 PR 13-NOV-2001; 2001US-0331287P.
 XX
 PA (HUMA-) HUMAN GENOME SCT INC.
 XX
 PI Rosen CA, Ruben SM;
 XX
 P1 WPI; 2003-430516/40.
 DR N-PSDB; ADC739861.
 DR
 XX
 PT New human secreted polypeptide for diagnosing, preventing or treating
 PT hematopoietic or hematologic disorders (e.g. anemia), autoimmune
 PT disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer or
 PT atherosclerosis).
 XX
 PS Claim 16; SEQ ID NO 1229; 2272pp; English.
 XX
 CC The invention relates to a novel human secreted polypeptide comprising a
 CC defined sequence given in the specification. The polypeptide, nucleic
 CC acid molecule, antibody, agonist or antagonist of the invention may be
 CC useful for preparing a composition for diagnosing or treating a
 CC hemopoietic or haematologic disorder such as anemia, autoimmune
 CC disorders such as rheumatoid arthritis, inflammation, Grave's disease,
 CC diabetes, systemic lupus erythematosus or glomerulonephritis,
 CC neurodegenerative disorders including Parkinson's disease and Alzheimer's
 CC disease, wounds and hyperproliferative disorders including
 CC atherosclerosis or cancer, as well as bacterial, viral, fungal or
 CC parasitic infections. The polypeptide may also be used during gene
 CC therapy procedures and for identifying a binding partner by contacting
 CC the polypeptide with a binding partner and determining whether the
 CC binding partner increases or decreases the activity of the polypeptide.
 CC The current sequence is that of the human secreted protein of the
 CC invention.
 CC
 XX
 SQ Sequence 462 AA;
 XX
 Query Match 87.3%; Score 2404; DB 7; Length 462;
 Best Local Similarity 88.1%; Pred. No. 5.5e-208;
 Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;
 QY 1 MRLRRLKRTWPLEVEPTLGHLSRLSLCTWGSSTRTPTITINYDPLTGE 60
 DB 1 MRLRRLKRTWPLEVEPTLGHLSRLSLCTWGSSTRTPTITINYDPLTGE 60
 QY 61 ETLASVIGGDLICLLQDDIPAPNTPSSTDSHSLQNNQPSLATSSNQTSWQDQDP 120
 DB 61 ETLASVIGGDLICLLQDDIPAPNTPSSTDSHSLQNNQPSLATSSNQTSWQDQDP 120

QY 121 SDSFQGAAGSGVWDDSMLGPSQNFEEAESIQDNHMAEGTGFPSEPMLCSESVGGVP 180
 DB 121 SDSFQGAAGSGVWDDSMLGPSQNFEEAESIQDNHMAEGTGFPSEPMLCSESVGGVP 180
 QY 181 HSELTLYGADCSANDLILVILHLMLESQYIPGCTEAKKLSMEKKKLSGVYLYQYM 240
 DB 181 HSELTLYGADCSANDLILVILHLMLESQYIPGCTEAKKLSMEKKKLSGVYLYQYM 240
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 DB 241 PLCESSATLTGVPVGNLIVNATLKINNEISVYKRLQLPESFICKERKGENVANIYKD 300
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 DB 263 -----ALNLPVPGVIVLPLEKTRIRPLDVRVSLISAVCR 300
 QY 361 DLFTASNDPLLMRFYLYADFRDNTVTVODTMKELYRKSHIQKESPKGRFVMLPSSSTH 420
 DB 301 DLFTASNDPLLMRFYLYADFRDNTVTVODTMKELYRKSHIQKESPKGRFVMLPSSSTH 360
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RESULT 15
 AAB35160
 ID AAB35160 strand: protein; 443 AA.
 AC AAB35160;
 XX
 DT 09-APR-2001 (first entry)
 DT
 XX
 DE Human Skp1-associated F-box protein-1 SAF-1alpha SEQ ID NO: 8.
 DE
 XX
 OS Homo sapiens.
 XX
 PN WC020077207-A2.
 XX
 PD 21-DEC-2000.
 XX
 PF 09-JUN-2000; 2000MO-US015873.
 XX
 PR 11-JUN-1999; 99US-00330517.
 XX
 PA (BURN-) BURNHAM INST.
 PA
 PI Reed JC, Matsuzawa S;
 XX
 DR WPI; 2001-071273/08.
 DR N-PSDB; AAC67284.
 XX
 PT Siah-Mediated Degradation Protein, useful for drug screening, for
 PT therapeutic applications and for functional genomics.
 PS Claim 15; Page 103-104; 121pp; English.
 XX
 CC The present invention provides the protein and coding sequences of
 CC several siah-mediated degradation proteins and SCF-complex proteins.
 CC These are designated Siah-1alpha, Siah-1 interacting protein (SIP), which
 CC encodes two proteins due to alternative splicing (SIP-L and SIP-S), Skp1-
 CC associated F-box protein-1alpha and beta and -2 (SAF-1alpha, SAF-1beta
 CC and SAF-2) and Skp1-associated destruction-box protein (SAD). The

CC proteins and their coding sequences are useful in the diagnosis and
CC treatment of cancers, disorders where too little cell division occurs
CC such as bone marrow aplasia, immunodeficiencies and inflammatory
CC diseases including sepsis, fibrosis, arthritis and graft versus host
CC disease

XX Sequence 443 AA;

Query Match 82.4%; Score 2270; DB 4; Length 443;

Best Local Similarity 99.8%; Pred. No. 6.7e-196;

Matches 430; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 152 QDNHMAEGTGFYSEPEMLCSESVGEQVPHSLFTLYOSADCSNDALIVLHILMLESG 211
Db 73 QDNHMAEGTGFYSEPEMLCSESVGEQVPHSLFTLYOSADCSNDALIVLHILMLESG 132
QY 212 YIPQTEKAKLSPEKWLSGVYKLQYMHPLCEGSSATLTCVPLGNLIVNATLKINNEI 271
Db 133 YIPQTEKAKLSPEKWLSGVYKLQYMHPLCEGSSATLTCVPLGNLIVNATLKINNEI 192
QY 272 RSVKRLQLLPESFCKEKLGENVANITYKDLQKLSRLFKDQIVYPLAFTQAALNLPVFG 331
Db 193 RSVKRLQLLPESFCKEKLGENVANITYKDLQKLSRLFKDQIVYPLAFTQAALNLPVFG 252
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Db 253 LVVLPLEIKIRIFRLLDVRSVLSLAVCRDIFASNDPLMRFYLRDPRDNTVRVODTD 312
QY 392 WKELVRKHIQKESPKGRFVMLPSSTHTIPFYPNPLHPPRPPSSRLPGIIGGEYDOR 451
Db 313 WKELVRKHIQKESPKGRFVMLPSSTHTIPFYPNPLHPPRPPSSRLPGIIGGEYDOR 372
QY 452 PTLFVGDPISSLLIPGCEIPSCQPPPLRPDPVGPPLPGPNPILPGRGPNDRPPFRPSR 511
Db 373 PTLFVGDPISSLLIPGCEIPSCQPPPLRPDPVGPPLPGPNPILPGRGPNDRPPFRPSR 432
QY 512 GRPTDGRLSFM 522
Db 433 GRPTDGRLSFM 443
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Search completed: November 16, 2004, 07:09:03
Job time : 159 secs

GenCore version 5.1.6
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OK protein - protein search, using sw model

Run on: November 16, 2004, 07:09:10 ; Search time 141 Seconds

(without alignments)
1309.864 Million cell updates/sec

Title: US-09-927-458-2

Perfect score: 2754
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 35381937 residues

Total number of hits satisfying chosen parameters: 1568699

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
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2	2754	100.0	522	14 US-10-245-593-2
3	2744	99.6	522	16 US-10-679-246-10
4	2489	90.4	482	13 US-10-042-417-14
5	2489	90.4	482	13 US-09-397-945-200
6	2404	87.3	462	15 US-10-264-237-2485
7	2404	87.3	462	15 US-10-653-595-200
8	2404	87.3	497	10 US-09-397-945-435
9	2404	87.3	443	16 US-10-679-246-8
10	2270	82.4	317	15 US-10-264-237-2484
11	1527	55.4	231	16 US-10-608-7654-752
12	1238	45.0	221	14 US-10-094-749-1723
13	1086	39.4	221	14 US-10-094-749-1723

14	714	25.9	174	10	US-09-397-945-434	Sequence 434, App
15	714	25.9	174	15	US-10-653-595-209	Sequence 209, App
16	714	25.9	174	15	US-10-653-595-434	Sequence 434, App
17	714	25.9	175	14	US-09-397-945-209	Sequence 209, App
18	396	14.4	76	14	US-10-029-386-27908	Sequence 27908, A
19	249	9.0	47	14	US-10-029-386-33496	Sequence 33496, A
20	215.5	7.8	500	17	US-10-739-930-9910	Sequence 9910, App
21	211	7.7	485	15	US-10-425-114-59910	Sequence 59910, A
22	207	7.5	485	15	US-10-425-114-59911	Sequence 59911, A
23	201	7.3	485	15	US-10-425-114-60984	Sequence 60984, A
24	198	7.2	447	17	US-10-425-115-349540	Sequence 349540, A
25	194	7.0	39	13	US-10-042-417-21	Sequence 21, App1
26	189	6.9	38	11	US-09-801-348-47	Sequence 47, App1
27	164	6.0	38	11	US-09-801-348-49	Sequence 49, App1
28	144	5.2	408	15	US-10-264-237-1835	Sequence 1835, App
29	142	5.2	1131	17	US-10-425-115-355048	Sequence 355048, App
30	140	5.1	379	15	US-10-264-049-2807	Sequence 2807, App
31	139	5.0	327	13	US-10-042-417-58	Sequence 58, App1
32	139	5.0	327	16	US-10-679-246-12	Sequence 12, App1
33	137	5.0	664	16	US-10-437-963-176808	Sequence 176808, App1
34	129.5	4.7	197	17	US-10-425-115-356769	Sequence 356769, App1
35	126	4.6	344	14	US-10-061-043A-27	Sequence 27, App1
36	126	4.6	344	14	US-10-060-634C-27	Sequence 27, App1
37	126	4.6	355	14	US-10-061-043A-35	Sequence 35, App1
38	126	4.6	355	14	US-10-060-634C-35	Sequence 35, App1
39	126	4.6	355	14	US-10-094-749-2883	Sequence 2883, App
40	125.5	4.6	754	16	US-10-437-963-134895	Sequence 134895, App
41	125	4.5	168	15	US-10-424-599-190794	Sequence 190794, App
42	125	4.5	204	15	US-10-424-599-283065	Sequence 283065, App
43	123.5	4.5	1827	16	US-10-437-963-158691	Sequence 158691, App
44	120.5	4.4	133	17	US-10-425-115-352606	Sequence 352606, App
45	120	4.4	684	16	US-10-687-732-23	Sequence 23, App1

ALIGNMENTS

RESULT 1
US-09-927-458-2
Sequence 2, Application US/09927458
Patent No. US20020058024A1
GENERAL INFORMATION:

APPLICANT: KOVACHENKO, David
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF RECEPTORS OF THE TNF/NGF RECEPTOR F2
FILE REFERENCE: WALLACH=22A
CURRENT APPLICATION NUMBER: US/09/927,458
CURRENT FILING DATE: 2001-08-13
PRIORITY APPLICATION NUMBER: PCT/IL98/00125
PRIORITY FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: IL 120485
PRIOR FILING DATE: 1997-03-19
PRIOR APPLICATION NUMBER: 09/381,358
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 522
TYPE: PRT
ORGANISM: Homo sapiens
US-09-927-458-2

Query Match 100.0%; Score 2754; DB 9; Length 522;
Best Local Similarity 100.0%; Pred. No. 4.9e-223;
Matches 522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 ETLASGYIVSGDLICLILODDIPAPNIPSTSESHSLQNNQPSLATSSNOTSMODEQP 120
QY 121 SDSFOGQAAGVWVNDSDMLGPSQNFPAESIQDNAAHAAEGTGYPSPMLCSSEVGGVP 180
Db 121 SDSFOGQAAGVWVNDSDMLGPSQNFPAESIQDNAAHAAEGTGYPSPMLCSSEVGGVP 180
QY 181 HSELTIVQSADCSANDALIVLHLMLESGYIPQTEAKALSMPEKMLSGVYKLOVMH 240
Db 181 HSELTIVQSADCSANDALIVLHLMLESGYIPQTEAKALSMPEKMLSGVYKLOVMH 240
QY 241 PLCEGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLLPESTICEKLGENVANIYKD 300
Db 241 PLCEGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLLPESTICEKLGENVANIYKD 300
QY 301 LOKLSRLFKDQIVYPLAFTRQALNPVFGVLVPLELKRIFRLLDVRSVLSAVCR 360
Db 301 LOKLSRLFKDQIVYPLAFTRQALNPVFGVLVPLELKRIFRLLDVRSVLSAVCR 360
QY 361 DLFTASNDPLMLRFLYLDRFDNTVRVQDTWKELYKRKHIOREKSPKGRFVMLPSTH 420
Db 361 DLFTASNDPLMLRFLYLDRFDNTVRVQDTWKELYKRKHIOREKSPKGRFVMLPSTH 420
QY 421 TTFYFNPPLHRRPFPSSSLPGIIGGEYDQRPPLVYGDPISSLIPOGGETPSQFPPLRP 480
Db 421 TTFYFNPPLHRRPFPSSSLPGIIGGEYDQRPPLVYGDPISSLIPOGGETPSQFPPLRP 480
QY 481 RFDVPGPLGPNPILPGRGPNDRFPFRPSKGRPTDRLSFM 522
Db 481 RFDVPGPLGPNPILPGRGPNDRFPFRPSKGRPTDRLSFM 522

RESULT 2

US-10-245-593-2
Sequence 2, Application US/10245593
Publication No. US20030039646A1

GENERAL INFORMATION:

APPLICANT: WALLACH, David
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF RECEPTORS OF THE TNF/NGF RECEPTOR
FILE REFERENCE: WALLACH=22A
CURRENT APPLICATION NUMBER: US/10/245,593
CURRENT FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: US/09/927,456
PRIOR FILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: PCT/IL98/00125
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: IL 120485
PRIOR FILING DATE: 1997-03-19
PRIOR APPLICATION NUMBER: 09/381,358
PRIOR FILING DATE: 1999-09-20
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 522
TYPE: PRT
ORGANISM: Homo sapiens
US-10-245-593-2

Query Match 100.0%; Score 2754; DB 14; Length 522;
Best Local Similarity 100.0%; Pred. No. 4,9e-223;
Matches 522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRLVRLKRTWPLVPEPTETLGHLSRLSLCTWGYSSNTRFTTLNFKDPLTQDE 60
Db 1 MLRLVRLKRTWPLVPEPTETLGHLSRLSLCTWGYSSNTRFTTLNFKDPLTQDE 60
QY 61 ETLASGYIVSGDLICLILODDIPAPNIPSTSESHSLQNNQPSLATSSNOTSMODEQP 120
Db 61 ETLASGYIVSGDLICLILODDIPAPNIPSTSESHSLQNNQPSLATSSNOTSMODEQP 120
QY 121 SDSFOGQAAGVWVNDSDMLGPSQNFPAESIQDNAAHAAEGTGYPSPMLCSSEVGGVP 180
Db 121 SDSFOGQAAGVWVNDSDMLGPSQNFPAESIQDNAAHAAEGTGYPSPMLCSSEVGGVP 180

Db 121 SDSFOGQAAGVWVNDSDMLGPSQNFPAESIQDNAAHAAEGTGYPSPMLCSSEVGGVP 180
QY 181 HSELTIVQSADCSANDALIVLHLMLESGYIPQTEAKALSMPEKMLSGVYKLOVMH 240
Db 181 HSELTIVQSADCSANDALIVLHLMLESGYIPQTEAKALSMPEKMLSGVYKLOVMH 240
QY 241 PLCEGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLLPESTICEKLGENVANIYKD 300
Db 241 PLCEGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLLPESTICEKLGENVANIYKD 300
QY 301 LOKLSRLFKDQIVYPLAFTRQALNPVFGVLVPLELKRIFRLLDVRSVLSAVCR 360
Db 301 LOKLSRLFKDQIVYPLAFTRQALNPVFGVLVPLELKRIFRLLDVRSVLSAVCR 360
QY 361 DLFTASNDPLMLRFLYLDRFDNTVRVQDTWKELYKRKHIOREKSPKGRFVMLPSTH 420
Db 361 DLFTASNDPLMLRFLYLDRFDNTVRVQDTWKELYKRKHIOREKSPKGRFVMLPSTH 420
QY 421 TTFYFNPPLHRRPFPSSSLPGIIGGEYDQRPPLVYGDPISSLIPOGGETPSQFPPLRP 480
Db 421 TTFYFNPPLHRRPFPSSSLPGIIGGEYDQRPPLVYGDPISSLIPOGGETPSQFPPLRP 480
QY 481 RFDVPGPLGPNPILPGRGPNDRFPFRPSKGRPTDRLSFM 522
Db 481 RFDVPGPLGPNPILPGRGPNDRFPFRPSKGRPTDRLSFM 522

RESULT 3

US-10-679-246-10
Sequence 10, Application US/10679246
Publication No. US20040163138A1

GENERAL INFORMATION:

APPLICANT: Reed, John C.
TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved
FILE REFERENCE: 66821-235
CURRENT APPLICATION NUMBER: US/10/679,246
CURRENT FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 09/591,694
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 522
TYPE: PRT
ORGANISM: Homo sapien
US-10-679-246-10

Query Match 99.6%; Score 2744; DB 16; Length 522;
Best Local Similarity 99.6%; Pred. No. 3,4e-222;
Matches 520; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLRLVRLKRTWPLVPEPTETLGHLSRLSLCTWGYSSNTRFTTLNFKDPLTQDE 60
Db 1 MLRLVRLKRTWPLVPEPTETLGHLSRLSLCTWGYSSNTRFTTLNFKDPLTQDE 60
QY 61 ETLASGYIVSGDLICLILODDIPAPNIPSTSESHSLQNNQPSLATSSNOTSMODEQP 120
Db 61 ETLASGYIVSGDLICLILODDIPAPNIPSTSESHSLQNNQPSLATSSNOTSMODEQP 120
QY 121 SDSFOGQAAGVWVNDSDMLGPSQNFPAESIQDNAAHAAEGTGYPSPMLCSSEVGGVP 180
Db 121 SDSFOGQAAGVWVNDSDMLGPSQNFPAESIQDNAAHAAEGTGYPSPMLCSSEVGGVP 180
QY 181 HSELTIVQSADCSANDALIVLHLMLESGYIPQTEAKALSMPEKMLSGVYKLOVMH 240
Db 181 HSELTIVQSADCSANDALIVLHLMLESGYIPQTEAKALSMPEKMLSGVYKLOVMH 240
QY 241 PLCEGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLLPESTICEKLGENVANIYKD 300
Db 241 PLCEGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLLPESTICEKLGENVANIYKD 300

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Page 3

QY 301 LQKSLRFLKQOLVPLLAFTROALNLPDVGVLVPLLELKLRIFFRLDVRSLVSLAVCR 360
Db 301 LQKSLRFLKQOLVPLLAFTROALNLPDVGVLVPLLELKLRIFFRLDVRSLVSLAVCR 360
QY 361 DLFTASNDPLMLRFLYLRDPDRNTVRVODDMKELYKRRHQRKESPKGFVLLPSSSTH 420
Db 361 DLFTASNDPLMLRFLYLRDPDRNTVRVODDMKELYKRRHQRKESPKGFVLLPSSSTH 420
QY 421 TIFPYNPMLHRPPSSRLPPGIIIGGEYDORFTLPHYGDPISSLIIPGGETPSQFPLRP 480
Db 421 TIFPYNPMLHRPPSSRLPPGIIIGGEYDORFTLPHYGDPISSLIIPGGETPSQFPLRP 480
QY 481 RFDVPGPLPGPNPILPGRGGNDRPFRPSRGRPTDRLSPM 522
Db 481 RFDVPGPLPGPNPILPGRGGNDRPFRPSRGRPTDRLSPM 522

RESULT 4
US-10-042-417-14
; Sequence 14: Application US/10042417
; Publication No. US20020123082A1
; GENERAL INFORMATION:
; APPLICANT: Paganio, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/10/042,417
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-15
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-042-417-14

Query Match 90.4%; Score 2489; DB 13; Length 482;
Best Local Similarity 98.1%; Pred. No. 9,4e-201;
Matches 472; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
QY 42 SNRFTTLNKKDPLTDEETLASVIGSDILCLIQDDIPAPNIPSSSTDSHSSLONN 101
Db 2 SNRFTTLNKKDPLTDEETLASVIGSDILCLIQDDIPAPNIPSSSTDSHSSLONN 101
QY 102 EOPSLATSSNOTSQMODROPDSFQGAAGSWNDDSMLEPSONFEAESIQDNAMHAEFT 161
Db 62 EOPSLATSSNOTSQMODROPDSFQGAAGSWNDDSMLEPSONFEAESIQDNAMHAEFT 121
QY 162 GFYSESEMLCSSEVGEVPHSLFTLYQSADCSANDALIVLIHLMLSEGYIPQTEAKA 221
Db 122 GFYSESEMLCSSEVGEVPHSLFTLYQSADCSANDALIVLIHLMLSEGYIPQTEAKA 181
QY 222 LSMEXKMLSGVYKLOQTMHPCGESSATLTVCVPGNLIIVNATLKINNRISYKALQLLP 281
Db 182 LSMEXKMLSGVYKLOQTMHPCGESSATLTVCVPGNLIIVNATLKINNRISYKALQLLP 241
QY 282 ESFICKCKLGENVANIKYDKLQSLRFLKQOLVPLLAFTROALNLPDVGVLVPLLELKL 341
Db 242 ESFICKCKLGENVANIKYDKLQSLRFLKQOLVPLLAFTROALNLPDVGVLVPLLELKL 301
QY 342 RIFRLDVRSLVSLAVCRDLFTASNDPLMLRFLYLRDPDRNTVRVODDMKELYKRRH 401
Db 302 RIFRLDVRSLVSLAVCRDLFTASNDPLMLRFLYLRDPDRNTVRVODDMKELYKRRH 361
QY 402 QRKSPSPGRFVLMPLPSTHTTIFYPNPMLHRPPSSRLPPGIIIGGEYDORFTLPHYGDPI 461
Db 362 QRKSPSPGRFVLMPLPSTHTTIFYPNPMLHRPPSSRLPPGIIIGGEYDORFTLPHYGDPI 421
QY 462 SSLLIPGGETPSQFPLRPFRDVPVGPLPGPNPILPGRGGNDRPFRPSRGRPTDRLSPM 521
Db 422 SSLLIPGGETPSQFPLRPFRDVPVGPLPGPNPILPGRGGNDRPFRPSRGRPTDRLSPM 481

QY 522 M 522
Db 482 M 482

RESULT 5
US-09-397-945-200
; Sequence 200: Application US/09397945
; Publication No. US20030065139A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: 95 Human secreted proteins
; FILE REFERENCE: P2027P1
; CURRENT APPLICATION NUMBER: US/09/397,945
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: PCT/US99/05804
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/078,566
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,576
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,573
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,574
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,579
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/080,314
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080,312
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/078,578
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,581
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,577
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,563
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/080,313
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 470
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 200
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (115)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-397-945-200

Query Match 87.3%; Score 2404; DB 10; Length 462;
Best Local Similarity 88.1%; Pred. No. 1.3e-193;
Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;

QY 1 MLRLRLLKRTPLVPEPEPTLGLHSLRLSLCTGYSSNRFITTLNKKDPLTDE 60
Db 1 MLRLRLLKRTPLVPEPEPTLGLHSLRLSLCTGYSSNRFITTLNKKDPLTDE 60
QY 61 ETLASVIGSDILCLIQDDIPAPNIPSSSTDSHSSLONNQPSLATSSNOTSQMODOP 120
Db 61 ETLASVIGSDILCLIQDDIPAPNIPSSSTDSHSSLONNQPSLATSSNOTSQMODOP 120
QY 121 SPSFQGAAGSWNDDSMLEPSONFEAESIQDNAMHAEFTGFYSEBMLCSSEVGEV 180
Db 121 SPSFQGAAGSWNDDSMLEPSONFEAESIQDNAMHAEFTGFYSEBMLCSSEVGEV 180
QY 181 HSLFTLYQSADCSANDALIVLIHLMLSEGYIPQTEAKALSMPEKMLSGVYKLOQTMH 240
Db 181 HSLFTLYQSADCSANDALIVLIHLMLSEGYIPQTEAKALSMPEKMLSGVYKLOQTMH 240

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OY 241 PLCEGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLLPESFICKELGENVANITYKD 300
DB 241 PLGSSATLTCVPLGNLIVN----- 262
OY 301 LQKLSRLPKQDLVPLAFTQALNLPDVGLVYLPLELTKRTIRLLDVSVLSAVCR 360
DB 263 -----ALNLPDVGLVYLPLELTKRTIRLLDVSVLSAVCR 300
OY 361 DLFTASNDPLMLRFLYLRFEDNTVRVODTWMKELYRKSHIQKXSPKGRFVMLPSTH 420
DB 301 DLFTASNDPLMLRFLYLRFEDNTVRVODTWMKELYRKSHIQKXSPKGRFVMLPSTH 360
OY 421 TTFYPNPLHRRPPSSRLPPGIIIGGEYDQRPPLPYVGDPISSLIPGGEFPSPPLRP 480
DB 361 TTFYPNPLHRRPPSSRLPPGIIIGGEYDQRPPLPYVGDPISSLIPGGEFPSPPLRP 420
OY 481 RFDVGPPLPGPNPLPGRGGNDRFPFRPSRGRPTDRLSPM 522
DB 421 RFDVGPPLPGPNPLPGRGGNDRFPFRPSRGRPTDRLSPM 462

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RESULT 6

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US-10-264-237-2485
; Sequence 2485, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Biese et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT FILING DATE: 2002-10-04
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: Patent In Ver. 3.1
; SEQ ID NO 2485
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (115)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-237-2485

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Query Match 87.3%; Score 2404; DB 15; Length 462;
Best Local Similarity 88.1%; Pred. No. 1.3e-193;
Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;

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OY 1 MLRLVRLKRTMPLEVPETPTLGLHRSRLSLCTGYSNTRFTTLNFKDPLTGD 60
DB 1 MLRLVRLKRTMPLEVPETPTLGLHRSRLSLCTGYSNTRFTTLNFKDPLTGD 60
OY 61 ETLASGYISGDLICLILODDIPAPNIPSTDSSEHSSIQNNEQPSLATSSNQTSXODEOP 120
DB 61 ETLASGYISGDLICLILODDIPAPNIPSTDSSEHSSIQNNEQPSLATSSNQTSXODEOP 120
OY 121 SPSFGQAAGSVMNDSDMLGSPQNFEEASTIQDNNAHMAEGTFPSEPMCLSESEVEQVP 180
DB 121 SPSFGQAAGSVMNDSDMLGSPQNFEEASTIQDNNAHMAEGTFPSEPMCLSESEVEQVP 180
OY 181 HSLFTLYOSADCSNDALIVLHLLMLSGYIPDGTAKALSMPEKWLSGVYKLOYM 240
DB 181 HSLFTLYOSADCSNDALIVLHLLMLSGYIPDGTAKALSMPEKWLSGVYKLOYM 240
OY 241 PLCEGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLPESPICKELGENVANITYKD 300
DB 241 PLCEGSSATLTCVPLGNLIVN----- 262
OY 301 LQKLSRLPKQDLVPLAFTQALNLPDVGLVYLPLELTKRTIRLLDVSVLSAVCR 360

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DB 263 -----ALNLPDVGLVYLPLELTKRTIRLLDVSVLSAVCR 300
OY 361 DLFTASNDPLMLRFLYLRFEDNTVRVODTWMKELYRKSHIQKXSPKGRFVMLPSTH 420
DB 301 DLFTASNDPLMLRFLYLRFEDNTVRVODTWMKELYRKSHIQKXSPKGRFVMLPSTH 360
OY 421 TTFYPNPLHRRPPSSRLPPGIIIGGEYDQRPPLPYVGDPISSLIPGGEFPSPPLRP 480
DB 361 TTFYPNPLHRRPPSSRLPPGIIIGGEYDQRPPLPYVGDPISSLIPGGEFPSPPLRP 420
OY 481 RFDVGPPLPGPNPLPGRGGNDRFPFRPSRGRPTDRLSPM 522
DB 421 RFDVGPPLPGPNPLPGRGGNDRFPFRPSRGRPTDRLSPM 462

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RESULT 7

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US-10-653-595-200
; Sequence 200, Application US/10653595
; Publication No. US20040048304A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 95 Human secreted proteins
; FILE REFERENCE: P2027P1C1
; CURRENT FILING DATE: 2003-09-03
; PRIOR FILING DATE: 2003-09-03
; PRIOR APPLICATION NUMBER: US 09/397945
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US99/05804
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/078,566
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,576
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,573
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,574
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,579
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/080,314
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080,312
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/078,578
; PRIOR FILING DATE: 1998-03-19
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 470
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 200
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (115)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-653-595-200

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Query Match 87.3%; Score 2404; DB 15; Length 462;
Best Local Similarity 88.1%; Pred. No. 1.3e-193;
Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;

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OY 1 MLRLVRLKRTMPLEVPETPTLGLHRSRLSLCTGYSNTRFTTLNFKDPLTGD 60
DB 1 MLRLVRLKRTMPLEVPETPTLGLHRSRLSLCTGYSNTRFTTLNFKDPLTGD 60
OY 61 ETLASGYISGDLICLILODDIPAPNIPSTDSSEHSSIQNNEQPSLATSSNQTSXODEOP 120
DB 61 ETLASGYISGDLICLILODDIPAPNIPSTDSSEHSSIQNNEQPSLATSSNQTSXODEOP 120
OY 121 SPSFGQAAGSVMNDSDMLGSPQNFEEASTIQDNNAHMAEGTFPSEPMCLSESEVEQVP 180
DB 121 SPSFGQAAGSVMNDSDMLGSPQNFEEASTIQDNNAHMAEGTFPSEPMCLSESEVEQVP 180

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Db 121 SDSFGQAAGGVWVNDSDMLGPSQNFESIQDNAMAEGETGYPSPHMLCSSEVSGVP 180
Qy 181 HSELTLYQSADCSANDALIVLHLMLESQYIPQGTAKALSMPEKMKLSGYKLCQYMH 240
Db 181 HSELTLYQSADCSANDALIVLHLMLESQYIPQGTAKALSMPEKMKLSGYKLCQYMH 240
Qy 241 PLCEGSSATLTCVPLGNLIYVNAITKINNEIRSVKRLQLPESFICKKLGENVANIYKD 300
Db 241 PLCEGSSATLTCVPLGNLIYVNAITKINNEIRSVKRLQLPESFICKKLGENVANIYKD 300
Qy 301 LQKLSRLFKDQLYVPLAFTROALNLPDVFGVLVPLLEKLRIFFLLDVRSVLSAVCR 360
Db 263 -----ALNLPDVFGVLVPLLEKLRIFFLLDVRSVLSAVCR 300
Qy 361 DLFTASNDPLLMRFYLDRFRDNTVRYQDTWKELVYKRIQKESPKGRFVWMLPSSTH 420
Db 301 DLFTASNDPLLMRFYLDRFRDNTVRYQDTWKELVYKRIQKESPKGRFVWMLPSSTH 360
Qy 421 TTFYPNPLHRRPPSSRLPPGIIIGGEYDQPTLPYVGDPISSLLPGGFTPSQFPPLRP 480
Db 361 TTFYPNPLHRRPPSSRLPPGIIIGGEYDQPTLPYVGDPISSLLPGGFTPSQFPPLRP 420
Qy 481 RFDVPGLPGPNPLIPGRGPNDRFPFRSGRPTDGRLSFM 522
Db 421 RFDVPGLPGPNPLIPGRGPNDRFPFRSGRPTDGRLSFM 462

RESULT 8
US-09-397-945-435

/ Sequence 435, Application US/09397945
/ Publication No. US2003065139A1
/ GENERAL INFORMATION:
/ APPLICANT: Human Genome Sciences, Inc. et al.
/ TITLE OF INVENTION: 95 Human secreted proteins
/ FILE REFERENCE: P2027P1
/ CURRENT APPLICATION NUMBER: US/09/397, 945
/ PRIOR APPLICATION NUMBER: PCT/US99/05804
/ PRIOR FILING DATE: 1999-09-17
/ PRIOR FILING DATE: 1999-03-18
/ PRIOR APPLICATION NUMBER: 60/078, 566
/ PRIOR FILING DATE: 1998-03-19
/ PRIOR APPLICATION NUMBER: 60/078, 576
/ PRIOR FILING DATE: 1998-03-19
/ PRIOR APPLICATION NUMBER: 60/078, 573
/ PRIOR FILING DATE: 1998-03-19
/ PRIOR APPLICATION NUMBER: 60/078, 574
/ PRIOR FILING DATE: 1998-03-19
/ PRIOR APPLICATION NUMBER: 60/078, 579
/ PRIOR FILING DATE: 1998-03-19
/ PRIOR APPLICATION NUMBER: 60/080, 314
/ PRIOR FILING DATE: 1998-04-01
/ PRIOR APPLICATION NUMBER: 60/080, 312
/ PRIOR FILING DATE: 1998-04-01
/ PRIOR APPLICATION NUMBER: 60/078, 578
/ PRIOR FILING DATE: 1998-03-19
/ PRIOR APPLICATION NUMBER: 60/078, 581
/ PRIOR FILING DATE: 1998-03-19
/ PRIOR APPLICATION NUMBER: 60/078, 577
/ PRIOR FILING DATE: 1998-03-19
/ PRIOR APPLICATION NUMBER: 60/078, 563
/ PRIOR FILING DATE: 1998-03-19
/ PRIOR APPLICATION NUMBER: 60/080, 313
/ PRIOR FILING DATE: 1998-04-01
/ NUMBER OF SEQ ID NOS: 470
/ SOFTWARE: Patentln Ver. 2.0
/ SEQ ID NO 435
/ LENGTH: 497
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: (150)
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-397-945-435

Query Match 87.3%; Score 2404; DB 10; Length 497;
Best Local Similarity 88.1%; Pred. No. 1,4e-193;
Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;
Qy 1 MELRVRLKRTMPLEVPETPEPTGLRSHLRSLICTGYSNNRFTTITNYKDPDITGDE 60
Db 36 MLRVRLKRTMPLEVPETPEPTGLRSHLRSLICTGYSNNRFTTITNYKDPDITGDE 95
Qy 61 ETLASGVISGDLICLLIIDDIPAPNIPSSSTDSSEHSLQNNQOESLATSNOTSQDEQP 120
Db 96 ETLASGVISGDLICLLIIDDIPAPNIPSSSTDSSEHSLQNNQOESLATSNOTSQDEQP 155
Qy 121 SDSFGQAAGGVWVNDSDMLGPSQNFESIQDNAMAEGETGYPSPHMLCSSEVSGVP 180
Db 156 SDSFGQAAGGVWVNDSDMLGPSQNFESIQDNAMAEGETGYPSPHMLCSSEVSGVP 215
Qy 181 HSELTLYQSADCSANDALIVLHLMLESQYIPQGTAKALSMPEKMKLSGYKLCQYMH 240
Db 216 HSELTLYQSADCSANDALIVLHLMLESQYIPQGTAKALSMPEKMKLSGYKLCQYMH 275
Qy 241 PLCEGSSATLTCVPLGNLIYVNAITKINNEIRSVKRLQLPESFICKKLGENVANIYKD 300
Db 276 PLCEGSSATLTCVPLGNLIYVNAITKINNEIRSVKRLQLPESFICKKLGENVANIYKD 297
Qy 301 LQKLSRLFKDQLYVPLAFTROALNLPDVFGVLVPLLEKLRIFFLLDVRSVLSAVCR 360
Db 298 -----ALNLPDVFGVLVPLLEKLRIFFLLDVRSVLSAVCR 335
Qy 361 DLFTASNDPLLMRFYLDRFRDNTVRYQDTWKELVYKRIQKESPKGRFVWMLPSSTH 420
Db 336 DLFTASNDPLLMRFYLDRFRDNTVRYQDTWKELVYKRIQKESPKGRFVWMLPSSTH 395
Qy 421 TTFYPNPLHRRPPSSRLPPGIIIGGEYDQPTLPYVGDPISSLLPGGFTPSQFPPLRP 480
Db 396 TTFYPNPLHRRPPSSRLPPGIIIGGEYDQPTLPYVGDPISSLLPGGFTPSQFPPLRP 455
Qy 481 RFDVPGLPGPNPLIPGRGPNDRFPFRSGRPTDGRLSFM 522
Db 456 RFDVPGLPGPNPLIPGRGPNDRFPFRSGRPTDGRLSFM 497

RESULT 9
US-10-653-595-435

/ Sequence 435, Application US/10653595
/ Publication No. US20040046304A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et. al.
/ TITLE OF INVENTION: 95 Human secreted proteins
/ FILE REFERENCE: P2027P1C1
/ CURRENT APPLICATION NUMBER: US/10/653, 595
/ PRIOR FILING DATE: 2003-09-03
/ PRIOR APPLICATION NUMBER: US 09/397945
/ PRIOR FILING DATE: 1999-09-17
/ PRIOR APPLICATION NUMBER: PCT/US99/05804
/ PRIOR FILING DATE: 1999-03-18
/ PRIOR APPLICATION NUMBER: 60/078, 566
/ PRIOR FILING DATE: 1998-03-19
/ PRIOR APPLICATION NUMBER: 60/078, 576
/ PRIOR FILING DATE: 1998-03-19
/ PRIOR APPLICATION NUMBER: 60/080, 314
/ PRIOR FILING DATE: 1998-04-01
/ PRIOR APPLICATION NUMBER: 60/080, 312
/ PRIOR FILING DATE: 1998-04-01
/ PRIOR APPLICATION NUMBER: 60/078, 578
/ PRIOR FILING DATE: 1998-03-19

Remaining Prior Application data removed - See file Wrapper or PALM.

NUMBER OF SEQ ID NOS: 470

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 435

LENGTH: 497

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SITE

LOCATION: (150)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-10-653-595-435

Query Match 87.3%; Score 2404; DB 15; Length 497;
Best Local Similarity 88.1%; Pred. No. 1,4e-193;
Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;

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QY 1 MRLPRLKRTWPEVETETPTLGHASHRLSLCTGWGSSNTRPITLTNYDPLTGP 60
DB 36 MRLVRLKRTWPEVETETPTLGHASHRLSLCTGWGSSNTRPITLTNYDPLTGP 95
QY 61 ETLASVIGSDLLICLLDIPAPNIPSSITDSEHSLONNEQSLATSSNQTSGODEP 120
DB 96 ETLASVIGSDLLICLLDIPAPNIPSSITDSEHSLONNEQSLATSSNQTSGODEP 155
QY 121 SDGFOGQAAGSGVNDSDMLGPSQNFEEASIQDNAMAEGETFPYSEPMICSESVGGV 180
DB 156 SDGFOGQAAGSGVNDSDMLGPSQNFEEASIQDNAMAEGETFPYSEPMICSESVGGV 215
QY 181 HSLTIVYQADCSANDALIVLHLMLESGYIPQGTAKALSMPEKMLSGYKIQYMH 240
DB 216 HSLTIVYQADCSANDALIVLHLMLESGYIPQGTAKALSMPEKMLSGYKIQYMH 275
QY 241 PLGEGSSATLTCPVLGNLIYVNAATLKINNEIRSVKRLQLIPESFICKELGENVANITYK 300
DB 276 PLGEGSSATLTCPVLGNLIYVNAATLKINNEIRSVKRLQLIPESFICKELGENVANITYK 297
QY 301 LQKLSRLFKDQVYPLAFTRQALNLPDVGFLVYLPLELKLRIPLLDVBSVLSAVCR 360
DB 298 -----ALNLPDVGFLVYLPLELKLRIPLLDVBSVLSAVCR 335
QY 361 DLFTASNDPLLMRLYLRDFEDNTTRVQDTWKELYKRKHIOREKSKGPFVMLPESST 420
DB 336 DLFTASNDPLLMRLYLRDFEDNTTRVQDTWKELYKRKHIOREKSKGPFVMLPESST 395
QY 421 TTPYVNPILHRPPSSRLPPGILIGGYDORPLPYVGDPPISSILPQGTSPSQFPLRP 480
DB 396 TTPYVNPILHRPPSSRLPPGILIGGYDORPLPYVGDPPISSILPQGTSPSQFPLRP 455
QY 481 RFDVGPPLGPNPILPGRGPNDRFPFRPSKGRPTDGRLSFM 522
DB 456 RFDVGPPLGPNPILPGRGPNDRFPFRPSKGRPTDGRLSFM 497

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RESULT 10

US-10-679-246-8

Sequence 8, Application US/10679246

Publication No. US20040163138A1

GENERAL INFORMATION:

APPLICANT: Reed, John C.

APPLICANT: Matsuzawa, Shu-ichi

TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved

FILE REFERENCE: 66821-235

CURRENT FILING DATE: 2003-10-02

PRIOR FILING DATE: 2000-06-09

NUMBER OF SEQ ID NOS: 50

SOFTWARE: FastSeq for Windows Version 4.0

LENGTH: 443

TYPE: PRT

ORGANISM: Homo sapien

US-10-679-246-8

Query Match

Best Local Similarity 99.8%; Pred. No. 2,4e-182;

Matches 430; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 92 DSEHSSLONNEQPSLATSSNQTSGODEPSPSGFOQAAGSGVNDSDMLGPSQNFEEASI 151
DB 13 DSEHSSLONNEQPSLATSSNQTSGODEPSPSGFOQAAGSGVNDSDMLGPSQNFEEASI 72
QY 152 QDNAMAEGETFPYSEPMICSESVGGVPHLETLVYQADCSANDALIVLHLMLESG 211
DB 73 QDNAMAEGETFPYSEPMICSESVGGVPHLETLVYQADCSANDALIVLHLMLESG 132
QY 212 YIPQGTAKALSMPEKMLSGYKIQYMHPLCESSATLTCPVLGNLIYVNAATLKINNEI 271
DB 133 YIPQGTAKALSMPEKMLSGYKIQYMHPLCESSATLTCPVLGNLIYVNAATLKINNEI 192
QY 272 RSVKRLQLIPESFICKELGENVANITYKDLKRLFDQQLVYPLAFTRQALNLPDVG 331
DB 193 RSVKRLQLIPESFICKELGENVANITYKDLKRLFDQQLVYPLAFTRQALNLPDVG 252
QY 332 LVVLPLELKLRIPLLDVRSVLSAVCRDLFTASNDPLLMRLYLRDFEDNTTRVQDT 391
DB 253 LVVLPLELKLRIPLLDVRSVLSAVCRDLFTASNDPLLMRLYLRDFEDNTTRVQDT 312
QY 392 WKELYKRKHIOREKSKGPFVMLPESSTHTTPTFPNPLHRPPSSRLPPGILIGGYDOR 451
DB 313 WKELYKRKHIOREKSKGPFVMLPESSTHTTPTFPNPLHRPPSSRLPPGILIGGYDOR 372
QY 452 PTLPYVGPPISSILPQGTSPSQFPLRPDRDPYGPPLIPGRGPNDRFPFRPSR 511
DB 373 PTLPYVGPPISSILPQGTSPSQFPLRPDRDPYGPPLIPGRGPNDRFPFRPSR 432
QY 512 GRPTDGRLSFM 522
DB 433 GRPTDGRLSFM 443

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RESULT 11

US-10-264-237-2484

Sequence 2484, Application US/10264237

Publication No. US20040009491A1

GENERAL INFORMATION:

APPLICANT: Birse et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PA13191

CURRENT FILING DATE: 2002-10-04

PRIOR FILING DATE: 2001-05-18

PRIOR FILING DATE: 2001-05-18

PRIOR FILING DATE: 2000-05-19

NUMBER OF SEQ ID NOS: 2876

SOFTWARE: PatentIn Ver. 3.1

SEQ ID NO 2484

LENGTH: 317

TYPE: PRT

ORGANISM: Homo sapiens

US-10-264-237-2484

Query Match 55.4%; Score 1527; DB 15; Length 317;
Best Local Similarity 94.0%; Pred. No. 6,1e-120;

Matches 300; Conservative 4; Mismatches 11; Indels 4; Gaps 2;

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QY 115 MDEQPSDSFOQAAGSGVNDSDMLGPSQNFEEASIQDNAMAEGETFPYSEPMICSES 174
DB 1 MDEQPSDSFOQAAGSGVNDSDMLGPSQNFEEASIQDNAMAEGETFPYSEPMICSES 60
QY 175 VEGOVPHSLTETLYQADCSANDALIVLHLMLESGYIPQGTAKALSMPEKMLSGY 234
DB 61 VEGOVPHSLTETLYQADCSANDALIVLHLMLESGYIPQGTAKALSMPEKMLSGY 120

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QY 235 KLOQMHPLCGSSKATLTCVPLGNLIVNATLKINNEIRSVKICOLLPESTICEKXGENV 294
DB 121 KLOQMHPLCGSSKATLTCVPLGNLIVNATLKINNEIRSVKICOLLPESTICEKXGENV 180
QY 295 ANIKYDQKLSRLFKDQVLYPLAFTRQALNLPDVEGLVLPLELKIRIFLLDVSYS 354
DB 181 ANIKYDQKLSRLFKDQVLYPLAFTRQALNLPDVEGLVLPLELKIRIFLLDVSYS 240
QY 355 LSACVCDLFTASNDPLLMRLYLADFPDNTVRVQDTWKELYKRKHIORESKGRF--V 412
DB 241 LSACVCDLFTASNDPLLMRLYLADFPDNTVRVQDTWKELYKRKHIORESKGRVCD 300
QY 413 MLPSSTHTIPFYNPPLHP 431
DB 301 PAIVNSHHSI--LSQPLAP 317
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RESULT 12
US-10-408-765A-752
; Sequence 752, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ. ID NOS: 3077
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 752
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-752
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Query Match 45.0%; Score 1238; DB 16; Length 231;
Best Local Similarity 100.0%; Pred. No. 8,7e-96;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 292 ENVANIYKDLQKLSRLFKDQVLYPLAFTRQALNLPDVEGLVLPLELKIRIFLLDVS 351
DB 1 ENVANIYKDLQKLSRLFKDQVLYPLAFTRQALNLPDVEGLVLPLELKIRIFLLDVS 60
QY 352 VLSISAVCRDLFTASNDPLLMRLYLADFPDNTVRVQDTWKELYKRKHIORESKGRF 411
DB 61 VLSISAVCRDLFTASNDPLLMRLYLADFPDNTVRVQDTWKELYKRKHIORESKGRF 120
QY 412 VMLPFSSTHTIPFYNPPLHPFPSSRLPGIIGGEYDQRTLPYVGDPISSLIPGGET 471
DB 121 VMLPFSSTHTIPFYNPPLHPFPSSRLPGIIGGEYDQRTLPYVGDPISSLIPGGET 180
QY 472 PSQFPPLRPFPDVPGLPGENPILPGRGPNDRFPFRSGRPTDGRLSFM 522
DB 181 PSQFPPLRPFPDVPGLPGENPILPGRGPNDRFPFRSGRPTDGRLSFM 231
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RESULT 13
US-10-094-749-1723
; Sequence 1723, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
```

```
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHITO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1723
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-1723
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Query Match 39.4%; Score 1086; DB 14; Length 221;
Best Local Similarity 93.1%; Pred. No. 5,2e-83;
Matches 203; Conservative 4; Mismatches 7; Indels 4; Gaps 1;
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QY 309 KQQLVYPLAFTR---QANLNPVYGLVLPLELKIRIFLLDVSLSISAVCRDLFT 364
DB 4 KQQLVYVIVYVLSLFLIALNLPDVEGLVLPLELKIRIFLLDVSLSISAVCRDLFT 63
QY 365 ASNDPLLMRLYLADFPDNTVRVQDTWKELYKRKHIORESKGRFVMLPSSSTHTIPF 424
DB 64 ASNDPLLMRLYLADFPDNTVRVQDTWKELYKRKHIORESKGRFVMLPSSSTHTIPF 123
QY 425 YNPPLHPFPSSRLPGIIGGEYDQRTLPYVGDPISSLIPGGETSOPPLRPFPDP 484
DB 124 YNPPLHPFPSSRLPGIIGGEYDQRTLPYVGDPISSLIPGGETSOPPLRPFPDP 183
QY 485 VGPLGPNPILPGRGPNDRFPFRSGRPTDGRLSFM 522
DB 184 VGPLGPNPILPGRGPNDRFPFRSGRPTDGRLSFM 221
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RESULT 14
US-09-397-945-434
; Sequence 434, Application US/09397945
; Publication No. US20030065139A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: 95 Human secreted proteins
; FILE REFERENCE: P2027P1
; CURRENT APPLICATION NUMBER: US/09/397,945
; CURRENT FILING DATE: 1999-03-17
; PRIOR APPLICATION NUMBER: PCT/US99/05804
; PRIOR FILING DATE: 1998-03-18
; PRIOR APPLICATION NUMBER: 60/078,566
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,576
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,573
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,574
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,579
; PRIOR FILING DATE: 1998-03-19
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; PRIOR APPLICATION NUMBER: 60/080,314
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080,312
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/078,578
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,581
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,577
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,563
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/080,313
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 470
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 434
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-397-945-434
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Query Match      25.9%; Score 714; DB 10; Length 174;
Best Local Similarity 100.0%; Pred. No. 8.3e-52;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 395 LYRKHIOKESPKGRFVMLLPSSHTTIPFYNPPLHPRPPSSRLPGIIGGEYDQRTL 454
    |||||
Db 47 LYRKHIOKESPKGRFVMLLPSSHTTIPFYNPPLHPRPPSSRLPGIIGGEYDQRTL 106
    |||||
QY 455 PYVGDPISSLIPGGETPSQFPPLRPDPVGPLPGPNLPGRGGPNDRPFRPSRGRP 514
    |||||
Db 107 PYVGDPISSLIPGGETPSQFPPLRPDPVGPLPGPNLPGRGGPNDRPFRPSRGRP 166
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QY 515 TDGRLSFM 522
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Db 167 TDGRLSFM 174
    |||||
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RESULT 15
US-10-653-595-209
; Sequence 209, Application US/10653595
; Publication No. US20040048304A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et. al.
; TITLE OF INVENTION: 95 Human secreted proteins
; FILE REFERENCE: P2027P1C1
; CURRENT FILING DATE: 2003-09-03
; PRIOR APPLICATION NUMBER: US/10/653,595
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: PCT/US99/05804
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/078,566
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,576
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,573
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,574
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,579
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/080,314
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080,312
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/078,578
; PRIOR FILING DATE: 1998-03-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 470
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 209
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; LENGTH: 174
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-653-595-209
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Query Match      25.9%; Score 714; DB 15; Length 174;
Best Local Similarity 100.0%; Pred. No. 8.3e-52;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 395 LYRKHIOKESPKGRFVMLLPSSHTTIPFYNPPLHPRPPSSRLPGIIGGEYDQRTL 454
    |||||
Db 47 LYRKHIOKESPKGRFVMLLPSSHTTIPFYNPPLHPRPPSSRLPGIIGGEYDQRTL 106
    |||||
QY 455 PYVGDPISSLIPGGETPSQFPPLRPDPVGPLPGPNLPGRGGPNDRPFRPSRGRP 514
    |||||
Db 107 PYVGDPISSLIPGGETPSQFPPLRPDPVGPLPGPNLPGRGGPNDRPFRPSRGRP 166
    |||||
QY 515 TDGRLSFM 522
    |||||
Db 167 TDGRLSFM 174
    |||||
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Job time : 143 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2004, 06:56:14 ; Search time 39 Seconds
(without alignments)
887,641 Million cell updates/sec

Title: US-09-927-458-2
Perfect score: 2754
Sequence: 1 MRLRVLLKRTWPLEVETPE.....DRFFPRSRGRPTDGLSTFW 522

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*
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3: /cgn2_6/ptodata/1/iaa/6A COMB pep.*
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5: /cgn2_6/ptodata/1/iaa/PCTUS COMB pep.*
6: /cgn2_6/ptodata/1/iaa/backfltest pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2744	99.6	522	US-09-591-694-10	Sequence 10, Appl
2	2489	90.4	482	US-09-385-219A-14	Sequence 16, Appl
3	2270	82.4	443	US-09-591-694-6	Sequence 8, Appl1
4	553	20.1	102	US-09-621-976-5935	Sequence 5935, Ap
5	194	7.0	39	US-09-385-219A-21	Sequence 21, Appl
6	189	6.9	38	US-09-172-841-47	Sequence 47, Appl
7	189	6.9	38	US-09-951-621-47	Sequence 47, Appl
8	164	6.0	38	US-09-172-841-49	Sequence 49, Appl
9	164	6.0	38	US-09-951-621-49	Sequence 49, Appl
10	144	5.0	321	US-09-166-350-15	Sequence 15, Appl
11	139	5.0	327	US-09-591-694-12	Sequence 12, Appl
12	139	5.0	327	US-09-385-219A-58	Sequence 58, Appl
13	117.5	4.3	503	US-09-599-287A-2	Sequence 2, Appl1
14	117	4.2	507	US-09-599-287A-24	Sequence 24, Appl1
15	112	4.1	690	US-09-248-796A-19169	Sequence 19169, A
16	110	4.0	424	US-09-538-092-1338	Sequence 1338, Ap
17	107.5	3.9	776	US-09-253-991A-28446	Sequence 28446, A
18	107	3.9	78	US-08-487-359-5	Sequence 5, Appl1
19	107	3.9	78	US-08-222-798A-5	Sequence 5, Appl1
20	107	3.9	489	US-09-543-681A-7388	Sequence 7388, Ap
21	105	3.8	297	US-09-253-991A-29217	Sequence 29217, A
22	104	3.8	1312	US-09-554-572-26	Sequence 26, Appl
23	103.5	3.8	79	US-08-487-359-8	Sequence 8, Appl1
24	103.5	3.8	79	US-08-222-798A-8	Sequence 8, Appl1
25	103.5	3.8	580	US-08-906-865-1	Sequence 1, Appl1
26	103.5	3.8	580	US-09-129-668-1	Sequence 1, Appl1
27	103.5	3.8	888	US-08-861-464-6	Sequence 6, Appl1

28	103.5	3.8	888	2	US-08-396-001-6	Sequence 6, Appl1
29	103.5	3.8	888	3	US-09-323-433A-6	Sequence 6, Appl1
30	103.5	3.8	888	4	US-09-826-752-6	Sequence 6, Appl1
31	103	3.7	133	4	US-09-252-991A-21490	Sequence 21490, A
32	103	3.7	431	4	US-09-248-796A-17260	Sequence 17260, A
33	102.5	3.7	79	1	US-08-487-359-2	Sequence 2, Appl1
34	102.5	3.7	79	1	US-08-222-798A-2	Sequence 2, Appl1
35	102.5	3.7	644	4	US-09-198-452A-822	Sequence 822, App
36	102	3.7	141	4	US-09-270-767-38716	Sequence 38716, A
37	102	3.7	141	4	US-09-270-767-53933	Sequence 53933, A
38	102	3.7	626	4	US-09-345-473E-43	Sequence 43, Appl
39	102	3.7	683	3	US-09-213-293D-1	Sequence 1, Appl1
40	102	3.7	866	4	US-09-527-084A-4	Sequence 4, Appl1
41	101.5	3.7	261	4	US-09-270-767-46755	Sequence 46755, A
42	101.5	3.7	1149	3	US-08-560-005-5	Sequence 5, Appl1
43	101.5	3.7	1149	3	US-09-418-540-5	Sequence 5, Appl1
44	101.5	3.7	1149	4	US-09-969-528-5	Sequence 5, Appl1
45	101	3.7	501	4	US-09-270-767-43743	Sequence 43743, A

ALIGNMENTS

RESULT 1
US-09-591-694-10
; Sequence 10, Application US/09591694
; Patent No. 6638734
; GENERAL INFORMATION:
; APPLICANT: Uom C. Reed
; APPLICANT: Shu-ichi Matsuzawa
; TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved
; TITLE OF INVENTION: in Protein Degradation, Products and Methods Related Thereo
; FILE REFERENCE: P-LJ 4220
; CURRENT APPLICATION NUMBER: US/09/591, 694
; CURRENT FILING DATE: 2000-06-09
; EARLIER APPLICATION NUMBER: US 09/330, 517
; EARLIER FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-591-694-10

Query Match	99.6%	Score 2744;	DB 4;	Length 522;
Best Local Similarity	99.6%	Pred. No. 36-255;		
Matches 520;	Conservative 1;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1	MRLRVLLKRTWPLEVETPEPTLGHLSHRSLICITWGYSSNTPFTTLNKKDPJTGDE	60	
DB	1	MRLRVLLKRTWPLEVETPEPTLGHLSHRSLICITWGYSSNTPFTTLNKKDPJTGDE	60	
QY	61	ETLASGYVSGDILICILDDIPAPNIPSTISEHSLONNEQPLATSNQTSMDPEP	120	
DB	61	ETLASGYVSGDILICILDDIPAPNIPSTISEHSLONNEQPLATSNQTSMDPEP	120	
QY	121	SOSFQQAQSSVWDDSMGLGPSQNFEBISIDNNAHMAEGTFYSEPMKCSSEVGGVP	180	
DB	121	SOSFQQAQSSVWDDSMGLGPSQNFEBISIDNNAHMAEGTFYSEPMKCSSEVGGVP	180	
QY	181	HSEFTLYGSAQSDNDALIVLHILMBSGYIPGTEKALSMEXKMLSGVYLQVYH	240	
DB	181	HSEFTLYGSAQSDNDALIVLHILMBSGYIPGTEKALSMEXKMLSGVYLQVYH	240	
QY	241	PLCEGSSATLTCVPLGNLIVNATLKINNEISVVRQLPLPSFICKEKLGENVANIYD	300	
DB	241	PLCEGSSATLTCVPLGNLIVNATLKINNEISVVRQLPLPSFICKEKLGENVANIYD	300	
QY	301	LQKLSLFDQVYPLIATFRQALNLPDVFGLVVPLEKLRIFLLDVRSLISAVCR	360	
DB	301	LQKLSLFDQVYPLIATFRQALNLPDVFGLVVPLEKLRIFLLDVRSLISAVCR	360	

QY 361 DLFTASNDPLLMRLFLYLDFPDNTVRVODTWMKELYRKRAHQRESEPKGRFVMLPESSTH 420
Db 361 DLFTASNDPLLMRLFLYLDFPDNTVRVODTWMKELYRKRAHQRESEPKGRFVMLPESSTH 420
QY 421 TTFEYVNDLHPRPFPSSRLPGIIGGEYDORPTLPYVGDPISSILPGSGEPSPQFPPLRP 480
Db 421 TTFEYVNDLHPRPFPSSRLPGIIGGEYDORPTLPYVGDPISSILPGSGEPSPQFPPLRP 480
QY 481 RFDVGPPLGPNPILPGRGPNDRPFRPSRGRPTDGRLSFM 522
Db 481 RFDVGPPLGPNPILPGRGPNDRPFRPSRGRPTDGRLSFM 522

RESULT 2

US-09-385-219A-14
; Sequence 14, Application US/09385219A
; Patent No. 6720181
; GENERAL INFORMATION:
; APPLICANT: Chiatour, D.
; APPLICANT: Pagano, M.
; APPLICANT: Laties, E.
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
; FILE REFERENCE: 5914-081
; CURRENT APPLICATION NUMBER: US/09/385,219A
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-385-219A-14

Query Match 90.4%; Score 2489; DB 4; Length 482;
Best Local Similarity 98.1%; Pred. No. 9.5e-231;
Matches 472; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 42 SNTRETTILNFKDPLTGTDEETLASGYISGDLICLILODDIPAPNIPESSTDESHSLQNN 101
Db 2 SNTRETTILNFKDPLTGTDEETLASGYISGDLICLILODDIPAPNIPESSTDESHSLQNN 61
QY 102 EOPSLATSSNOTSMODEQPSDSFOGQAQSGVWMDSDMLGSPQNFEEASIQDNHMAEGT 161
Db 62 EOPSLATSSNOTSIQDEQPSDSFOGQAQSGVWMDSDMLGSPQNFEEASIQDNHMAEGT 121
QY 162 GFYSPPEMLCSSEVGEQVPHSLLETLYQSGADCSANDALIVLHILMLESGYIPQGTBAKA 221
Db 122 GFYSPPEMLCSSEVGEQVPHSLLETLYQSGADCSANDALIVLHILMLESGYIPQGTBAKA 181
QY 222 LSMPEKWLKSGYKQYVHPLCEGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLLP 281
Db 182 LSMPEKWLKSGYKQYVHPLCEGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLLP 241
QY 282 ESFICEKELGENVANITYKDLQKLSLFDQOLVYPLLAFTROALNLDVYFGLVYPLBKL 341
Db 242 ESFICEKELGENVANITYKDLQKLSLFDQOLVYPLLAFTROALNLDVYFGLVYPLBKL 301
QY 342 RIFRLLDVRSVLSISAVCRDLFTASNDPLLMRLFLYLDFPDNTVRVODTWMKELYRKRAHI 401
Db 302 RIFRLLDVRSVLSISAVCRDLFTASNDPLLMRLFLYLDFPDNTVRVODTWMKELYRKRAHI 361
QY 402 QKRESEPKGRFVMLPESSTHTTIPFYVNPPLHPRPFPSSRLPGIIGGEYDORPTLPYVGDPI 461
Db 362 QKRESEPKGRFVMLPESSTHTTIPFYVNPPLHPRPFPSSRLPGIIGGEYDORPTLPYVGDPI 421
QY 462 SSLIPGEPTSPQFPPLRPFRDVPVGLPDPNPILPGRGPNDRPFRPSRGRPTDGRLSF 521
Db 521 SSLIPGEPTSPQFPPLRPFRDVPVGLPDPNPILPGRGPNDRPFRPSRGRPTDGRLSF 481

Db 422 SSLIPGEPTSPQFPPLRPFRDVPVGLPDPNPILPGRGPNDRPFRPSRGRPTDGRLSF 481
QY 522 M 522
Db 482 M 482

RESULT 3

US-09-591-694-8
; Sequence 8, Application US/09591694
; Patent No. 6638734
; GENERAL INFORMATION:
; APPLICANT: John C. Reed
; APPLICANT: Shu-ichi Matsuzawa
; TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved
; FILE REFERENCE: In Protein Degradation, Products and Methods Related Thereof
; FILE REFERENCE: P-Lt 4220
; CURRENT APPLICATION NUMBER: US/09/591,694
; PRIOR FILING DATE: 2000-06-09
; EARLIER APPLICATION NUMBER: US 09/330,517
; EARLIER FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 443
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-591-694-8

Query Match 82.4%; Score 2270; DB 4; Length 443;
Best Local Similarity 99.8%; Pred. No. 1e-209;
Matches 430; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 92 DSEHSLQNNRQPSLATSSNOTSMODEQPSDSFOGQAQSGVWMDSDMLGSPQNFEEASI 151
Db 13 DSEHSLQNNRQPSLATSSNOTSMODEQPSDSFOGQAQSGVWMDSDMLGSPQNFEEASI 72
QY 152 QDNHMAEGTGFYSPPEMLCSSEVGEQVPHSLLETLYQSGADCSANDALIVLHILMLESG 211
Db 73 QDNHMAEGTGFYSPPEMLCSSEVGEQVPHSLLETLYQSGADCSANDALIVLHILMLESG 132
QY 212 YIPQGTBAKALSMPEKWLKSGYKQYVHPLCEGSSATLTCVPLGNLIVNATLKINNEI 271
Db 133 YIPQGTBAKALSMPEKWLKSGYKQYVHPLCEGSSATLTCVPLGNLIVNATLKINNEI 192
QY 272 RSVKRLQLLPESFICEKELGENVANITYKDLQKLSLFDQOLVYPLLAFTROALNLDVYFGL 331
Db 193 RSVKRLQLLPESFICEKELGENVANITYKDLQKLSLFDQOLVYPLLAFTROALNLDVYFGL 252
QY 332 LVYPLBKLRLIFRLLDVRSVLSISAVCRDLFTASNDPLLMRLFLYLDFPDNTVRVODT 391
Db 253 LVYPLBKLRLIFRLLDVRSVLSISAVCRDLFTASNDPLLMRLFLYLDFPDNTVRVODT 312
QY 392 WKELYRKRAHQRESEPKGRFVMLPESSTHTTIPFYVNPPLHPRPFPSSRLPGIIGGEYDOR 451
Db 313 WKELYRKRAHQRESEPKGRFVMLPESSTHTTIPFYVNPPLHPRPFPSSRLPGIIGGEYDOR 372
QY 452 PTLFYVGDPISSILPGSGEPSPQFPPLRPFRDVPVGLPDPNPILPGRGPNDRPFRPSR 511
Db 373 PTLFYVGDPISSILPGSGEPSPQFPPLRPFRDVPVGLPDPNPILPGRGPNDRPFRPSR 432
QY 512 GRPTDGRLSFM 522
Db 433 GRPTDGRLSFM 443

RESULT 4

US-09-621-976-5935
; Sequence 5935, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.

APPLICANT: Giordano, J.V.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET, 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 5935
LENGTH: 102
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: UNSURE
LOCATION: 87
OTHER INFORMATION: Xaa = Cys, Gly
US-09-621-976-5935

Query Match 20.1%; Score 553; DB 4; Length 102;
Best Local Similarity 99.0%; Pred. No. 1,9e-45;
Matches 98; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 413 MLPLSSHTTTPFYNPPLHPRFPSSRLPPGIGGYDQPTLPYVGDPISSLIPGGETP 472
DB 1 MLPLSSHTTTPFYNPPLHPRFPSSRLPPGIGGYDQPTLPYVGDPISSLIPGGETP 60
QY 473 SQFPPLRPFPDVPGLPGPNPILPGRGQPNDRFPFRSR 511
DB 61 SQFPPLRPFPDVPGLPGPNPILPGRGQPNDRFPFRSR 99

RESULT 5
US-09-385-219A-21
Sequence 21, Application US/09385219A
Patent No. 6720181
GENERAL INFORMATION:
APPLICANT: Chiatour, D.
APPLICANT: Pagano, M.
APPLICANT: Latres, E.
TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
FILE REFERENCE: 5914-081
CURRENT APPLICATION NUMBER: US/09/385,219A
CURRENT FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: 60/098,355
PRIOR FILING DATE: 1998-08-28
PRIOR APPLICATION NUMBER: 60/118,568
PRIOR FILING DATE: 1999-02-03
PRIOR APPLICATION NUMBER: 60/124,449
PRIOR FILING DATE: 1999-03-15
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21
LENGTH: 39
TYPE: PRT
ORGANISM: Homo sapiens
US-09-385-219A-21

Query Match 7.0%; Score 194; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.5e-11;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 LPLELKRIFRLLDVRVSLSLAVCRDLFTASNDPLMW 373
DB 1 LPLELKRIFRLLDVRVSLSLAVCRDLFTASNDPLMW 39

RESULT 6
US-09-172-841-47
Sequence 47, Application US/09172841
Patent No. 623081
GENERAL INFORMATION:
APPLICANT: Harper, Jeffrey W.
APPLICANT: Elledge, Stephen J.
TITLE OF INVENTION: F-BOX PROTEINS AND GENES

FILE REFERENCE: BCM-03510
CURRENT APPLICATION NUMBER: US/09/172,841
CURRENT FILING DATE: 1998-10-15
EARLIER APPLICATION NUMBER: 08/951,621
EARLIER FILING DATE: 1997-10-16
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 47
LENGTH: 38
TYPE: PRT
ORGANISM: Homo sapiens
US-09-172-841-47

Query Match 6.9%; Score 189; DB 3; Length 38;
Best Local Similarity 100.0%; Pred. No. 4.3e-11;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 LPLELKRIFRLLDVRVSLSLAVCRDLFTASNDPLMW 372
DB 1 LPLELKRIFRLLDVRVSLSLAVCRDLFTASNDPLMW 38

RESULT 7
US-08-951-621-47
Sequence 47, Application US/08951621
Patent No. 6573094
GENERAL INFORMATION:
APPLICANT: HARPER, JEFFREY W.
APPLICANT: ELLEDGE, STEPHEN J.
TITLE OF INVENTION: F-BOX GENES AND PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/951,621
FILING DATE: 16-OCT-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: BCM-02999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-08-951-621-47

Query Match 6.9%; Score 189; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 4.3e-11;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 LPLELKRIFRLLDVRVSLSLAVCRDLFTASNDPLMW 372
DB 1 LPLELKRIFRLLDVRVSLSLAVCRDLFTASNDPLMW 38

RESULT 8

US-09-172-841-49
; Sequence 49, Application US/09172841
; Patent No. 6232081
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeffrey W.
; APPLICANT: Elledge, Stephen J.
; TITLE OF INVENTION: F-BOX PROTEINS AND GENES
; FILE REFERENCE: BCM-03510
; CURRENT APPLICATION NUMBER: US/09/172,841
; CURRENT FILING DATE: 1998-10-15
; EARLIER APPLICATION NUMBER: 08/951,621
; EARLIER FILING DATE: 1997-10-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-172-841-49
Query Match 6.0%; Score 164; DB 3; Length 38;
Best Local Similarity 86.8%; Pred. No. 1,1e-08;
Matches 33; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 335 LPLEIKRIFFRLDVRSLISAVCRDLFTASNDPLL 372
DB 1 LPLEIKRIFFRLDVRSLISAVCRDLFTASNDPLL 38
RESULT 9
US-08-951-621-49
; Sequence 49, Application US/08951621
; Patent No. 6573094
; GENERAL INFORMATION:
; APPLICANT: HARPER, JEFFREY W.
; APPLICANT: ELLEDGE, STEPHEN J.
; TITLE OF INVENTION: F-BOX GENES AND PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/951,621
; FILING DATE: 16-OCT-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: BCM-02999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: Protein
US-08-951-621-49
Query Match 6.0%; Score 164; DB 4; Length 38;
Best Local Similarity 86.8%; Pred. No. 1,1e-08;
Matches 33; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 335 LPLEIKRIFFRLDVRSLISAVCRDLFTASNDPLL 372
DB 1 LPLEIKRIFFRLDVRSLISAVCRDLFTASNDPLL 38
RESULT 10
US-09-166-350-15
; Sequence 15, Application US/09166350A
; Patent No. 6440663
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Chen, Yao
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Old, Lloyd
; APPLICANT: Jager, Elke
; APPLICANT: Knuth, Alex
; TITLE OF INVENTION: Renal Cancer Associated Antigens and
; FILE REFERENCE: 10461/7051
; CURRENT APPLICATION NUMBER: US/09/166,350A
; CURRENT FILING DATE: 1998-10-05
; EARLIER APPLICATION NUMBER: US 09/166,350
; EARLIER FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-166-350-15
Query Match 5.2%; Score 144; DB 4; Length 321;
Best Local Similarity 23.1%; Pred. No. 3e-05;
Matches 74; Conservative 47; Mismatches 90; Indels 110; Gaps 16;
QY 233 VKYQYMPHLECG--SSATLTCTVPL--GNLYVNAITKINNE-----IRSV-- 274
DB 35 MFRQMMFELAPGVSSNLENKPCPRARGSLQKTSADTKGQEOAKERAEFLKAVEE 94
QY 275 -----RRLDLP-----SFICKKIGENVANYI---KDLKLSRL---FK 309
DB 95 EONGALYEAIKFYRAMQVPEIEKITYTSSPDGDGNGSYIENDNDSDMADLSYFQ 154
QY 310 DQLYVELLAFTROALNL--PDV---FGVVLPELKRITRL-----LDVRSVLSAV 358
DB 155 QQ-----LTFQESVYKLCPHELSSQIHISVLPMEVLVIYFRWVWSSDLDRSLQSLV 209
QY 359 CRDLFTASNDPLLRFYLRDPRNTVR--VQDTDKKELYRKRIKESPKGRFVMLPS 417
DB 210 CGFYICARDPEIWMILACKVWGRCIKVYTSKRMFLER-----PVRFDGYIIS 262
QY 418 ST-----HTIPYPNLPMPRPFPSSRLPGIIGEXYDQRPFLPYVGD 460
DB 263 KTTYIROGROSLDGFYRAMHQVEY--RYIRFFPDGHV----- 298
QY 461 ISSLIPGPGETPSQPPPLRP 481
DB 299 --MULTPEEPOSIVRLRTR 317
RESULT 11
US-09-591-694-12
; Sequence 12, Application US/09591694
; Patent No. 6638734
; GENERAL INFORMATION:
; APPLICANT: John C. Reed
; APPLICANT: Shu-ichi Matsuzawa
; TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved
; FILE REFERENCE: P-LJ 4220
; CURRENT APPLICATION NUMBER: US/09/591,694
; CURRENT FILING DATE: 2000-06-09

EARLIER APPLICATION NUMBER: US 09/330,517
EARLIER FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 327
TYPE: PRT
ORGANISM: Homo sapien
US-09-591-694-12

Query Match 5.0%; Score 139; DB 4; Length 327;
Best Local Similarity 25.1%; Pred. No. 9.5e-05;
Matches 57; Conservative 32; Mismatches 64; Indels 74; Gaps 11;

QY 291 GENVANYI---KDLQKLSRL---FKDQVYPLLAFTROALNT---PDV---FGLVVLPL 337
DB 19 GDGVSNIYEDNDSDSKADLISYFQQQ---LTFGESVTKLQCPBELSSQIHISVLPM 73
QY 338 ELKLRIRL---LDVRSVLSAVGRDLFTASNDPLMRFLYLRDPNTRV-VQDD 391
DB 74 EVMYIRWVSSDLDRSLSEQLSLVGRGYICARDEIWRACLKMGSSCKLVPTYS 133
QY 392 WKELYRKRIQRKSPKGRFVMLLPSSST---HTIPYPNPLPRPF 434
DB 134 WREWFRLR-----PVRFDGVYISKTYIRQEGSLDGFYAMQVEY---RYIRFF 183
QY 435 PSSRLPGIIGGYDQRPFLPYVGDPLISLIPGGETPSQFPLRPP 481
DB 184 PDGHV-----MMLTPEEPQSIYPRLRTR 207

RESULT 12

US-09-385-219A-58
Sequence 58; Application US/09385219A
Patent No. 6720181
GENERAL INFORMATION:
APPLICANT: Chateau, D.
APPLICANT: Pasano, M.
APPLICANT: Latres, E.
TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
FILE REFERENCE: 5814-081
CURRENT APPLICATION NUMBER: US/09/385,219A
CURRENT FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: 60/098,355
PRIOR FILING DATE: 1998-08-28
PRIOR APPLICATION NUMBER: 60/118,568
PRIOR FILING DATE: 1999-02-03
PRIOR APPLICATION NUMBER: 60/124,449
PRIOR FILING DATE: 1999-03-15
NUMBER OF SEQ ID NOS: 90
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 58
LENGTH: 327
TYPE: PRT
ORGANISM: Homo sapiens
US-09-385-219A-58

Query Match 5.0%; Score 139; DB 4; Length 327;
Best Local Similarity 25.1%; Pred. No. 9.5e-05;
Matches 57; Conservative 32; Mismatches 64; Indels 74; Gaps 11;

QY 291 GENVANYI---KDLQKLSRL---FKDQVYPLLAFTROALNT---PDV---FGLVVLPL 337
DB 19 GDGVSNIYEDNDSDSKADLISYFQQQ---LTFGESVTKLQCPBELSSQIHISVLPM 73
QY 338 ELKLRIRL---LDVRSVLSAVGRDLFTASNDPLMRFLYLRDPNTRV-VQDD 391
DB 74 EVMYIRWVSSDLDRSLSEQLSLVGRGYICARDEIWRACLKMGSSCKLVPTYS 133
QY 392 WKELYRKRIQRKSPKGRFVMLLPSSST---HTIPYPNPLPRPF 434
DB 134 WREWFRLR-----PVRFDGVYISKTYIRQEGSLDGFYAMQVEY---RYIRFF 183

QY 435 PSSRLPGIIGGYDQRPFLPYVGDPLISLIPGGETPSQFPLRPP 481
DB 184 PDGHV-----MMLTPEEPQSIYPRLRTR 207

RESULT 13

US-09-599-287A-2
Sequence 2; Application US/09599287A
Patent No. 6635446
GENERAL INFORMATION:
APPLICANT: Narayanasamy Ramesh
APPLICANT: Ines M. Anton
APPLICANT: John H. Hartwig
APPLICANT: Raif S. Geba
TITLE OF INVENTION: WIP, A WASP-Associated Protein
FILE REFERENCE: 1242.1022-004
CURRENT APPLICATION NUMBER: US/09/599,287A
CURRENT FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: PCT/US98/27501
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/101,457
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/068,533
PRIOR FILING DATE: 1997-12-23
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 503
TYPE: PRT
ORGANISM: Human
US-09-599-287A-2

Query Match 4.3%; Score 117.5; DB 4; Length 503;
Best Local Similarity 33.1%; Pred. No. 0.023;
Matches 46; Conservative 9; Mismatches 41; Indels 43; Gaps 9;

QY 415 LPSSTHTIPYPNPLPRPPSSR---LPGIIGGYDQRPFLPYVGDPLISLIP 466
DB 294 VSTR--PSADHRHLAPPPSRGPPPLPSSGN--DETPRLPQNLSSSTPLP 349
QY 467 GBGET-----PSQPPPLRPPDP--VGPLPGPNPI-----LPG----- 497
DB 350 SPGRSGPLPPPSRPPPPVDDPPGSGPLPPPPVSSNGSTRALPATPOLPSSGVDS 409
QY 498 -RGPNDRF--PPRPRGRP 514
DB 410 PRSGRPPPLPPDRPSAGAP 428

RESULT 14

US-09-598-287A-24
Sequence 24; Application US/09599287A
Patent No. 6635446
GENERAL INFORMATION:
APPLICANT: Narayanasamy Ramesh
APPLICANT: Ines M. Anton
APPLICANT: John H. Hartwig
APPLICANT: Raif S. Geba
TITLE OF INVENTION: WIP, A WASP-Associated Protein
FILE REFERENCE: 1242.1022-004
CURRENT APPLICATION NUMBER: US/09/599,287A
CURRENT FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: PCT/US98/27501
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/101,457
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/068,533
PRIOR FILING DATE: 1997-12-23
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 24
LENGTH: 507
TYPE: PRT

```
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Translated WIP ORF No. 6635446 3
US-09-559-287A-24

Query Match
Best Local Similarity 4.2%; Score 117; DB 4; Length 507;
Matches 46; Conservative 9; Mismatches 41; Indels 44; Gaps 9;

QY 415 LPSTHTTFFVFNPLHPPPSR-----LPPGIGGEYDQRPFLPVGPISSL--IP 466
DB 297 VPSFPR--PSAPHRPHLRPPPSRPPPLPSSSGN--DETPRLPQRLNLSSTPPLP 352
QY 467 GPGET-----PSQFPLRPFRDP--VGPLPGNP-----LPG----- 497
DB 353 SPGRSGPLPPPVPSERPPPRVDPPGRSGPLPPPPVSRKGSSTRALPAPQLPSSSGVD 412
QY 498 --RGCPNDRF--PFRPSRGRP 514
DB 413 SPGRSGPLPPDRPSAGAP 432

RESULT 15
US-09-248-796A-19169
Sequence 19169, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstein et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248, 796A
PRIOR FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074, 725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096, 409
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 19169
LENGTH: 690
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-19169

Query Match
Best Local Similarity 4.1%; Score 112; DB 4; Length 690;
Matches 114; Conservative 76; Mismatches 189; Indels 192; Gaps 30;

QY 42 SNTREITLANKDPLTGDEET-----IASYGVSGDLICLLQDDIPAPIPST--DS 93
DB 166 SPPKASIALVVPDATEGTKESSIILALASLAKASGS-----NNETPPSSQSSSTNNNS 219
QY 94 EHSILQNNQPSLAT-----SSNQTSMDQEPSDSFGQAAGSG--VWND-- 137
DB 220 NNSNSNSNSGSGNATNIIQLSALGNSNTGSASQPPSQQYSSYPQGGGQAGNDLL 279
QY 138 SML-----GPSQNFEAESIQDNAMAE----- 159
DB 280 NMLQOMOGGGPTGASPASPVVGSNEARGPTAEFRRRGRDNEVGSQYGERNRSRSPKR 339
QY 160 GTGFYSPSPMLCSESEVEGVPHSLETTYQADCS-----DANDALIVLHILMLMSGYIP 214
DB 340 GSNITWVRSP--SSSVQA--LQNMGNLQKQKVHGVQNTNG-----QVDQGFVP 387
QY 215 QGTEKALSMPEKWKLSGVYKLQYMHPLCEGASATLTCVPLGNLIVNATIKI-----NN 269
DB 388 PNAMGELNLP-----GTPHYRPTVQFDSF--IPQGTVKVLSRTLFLGVPRNM 435
QY 270 EIRSVKRLQLLP-----ESFICKERKGENVANIY--KDLQKLSRLFKDQLVYPL-----LA 318
DB 436 DERSLAQV--LRPYALIQVILNSEKKAFAVKYISRRRAEQVITSFNKDGALPLATRWGVG 494
QY 319 F-TROALNLPDVFGIVLPLEIKLIRFL----- 346
```

```
DB 495 FGRPRCCNVQ--HGSIIPIQ-----RLTEADKNWIVHAQMGGTGGPILSGMVDEPD 546
QY 347 LDVRSVLSLAVCRDLFT--ASNDPLMRFLYLDFFRNTYRVQDTWKE--LYRKHHIQ 402
DB 547 IEIGSLSSKAWSKKMPNARSNGP-----KSNRGPBPDEEVKTTLLIPQDIQ 595
QY 403 RKSPKGRFVMLPSTHTTFFVFNPLHPPPSRRLPPGIGGEYDQRPFLPVGPISS 462
DB 596 MTHGAQPCQNTYLGSSV-----NPLQ-----GLFGNNPQQQQQCP--PPF 633
QY 463 SLIPGPGETPSQFPLRFRFPDVG--LPFPN 492
DB 634 PQPQPQPPMQFPAGFPQMPQOPGQPGKN 664

Search completed: November 16, 2004, 07:13:13
Job time : 40 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2004, 07:24:31 ; Search time 41 Seconds
(without alignments)

1225.004 Million cell updates/sec

Title: US-09-927-458-2

Sequence: 522
1 MRURVRLKRTMPLEVPETE.....DRPPRPSRGRPTDRLSPM 522

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database :

1: PIR79:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	1.5	353	2 T21616	hypothetical prote
2	8	1.5	572	2 B84648	hypothetical prote
3	7	1.3	25	2 S22221	peroxidase (EC 1.1
4	7	1.3	84	2 S76012	hypothetical prote
5	7	1.3	91	2 E86163	protein F15K9.18 l
6	7	1.3	96	2 B75134	hypothetical prote
7	7	1.3	110	2 B55863	excisionase - Stre
8	7	1.3	140	2 AH0243	4-carboxymuconolac
9	7	1.3	150	2 S73394	hypothetical prote
10	7	1.3	160	1 AFA1AC	allophycocyanin al
11	7	1.3	161	2 A31385	allophycocyanin al
12	7	1.3	167	2 F97162	hypothetical prote
13	7	1.3	184	2 AG1489	hypothetical prote
14	7	1.3	188	2 T26741	hypothetical prote
15	7	1.3	196	2 B87271	general secretion
16	7	1.3	216	2 AF2026	hypothetical prote
17	7	1.3	224	2 G72398	hypothetical prote
18	7	1.3	224	2 AH0875	probable membrane
19	7	1.3	229	2 F70800	probable transport
20	7	1.3	238	2 T04166	thiamin-like pro
21	7	1.3	243	2 D81804	hypothetical prote
22	7	1.3	246	2 T16371	hypothetical prote
23	7	1.3	257	2 A96033	probable thiamine
24	7	1.3	261	2 A60404	MHC class II histo
25	7	1.3	269	2 F69541	spermidine synthas
26	7	1.3	269	2 D84312	sulfate transport
27	7	1.3	273	2 T31506	hypothetical prote
28	7	1.3	278	2 B99415	hypothetical prote
29	7	1.3	291	2 S78602	peroxidase (EC 1.1

30	7	1.3	292	2 A47125	transcription acti
31	7	1.3	299	2 B95939	probable spermidin
32	7	1.3	304	2 C72324	homoserine O-succi
33	7	1.3	307	2 A83123	probable transcrip
34	7	1.3	310	2 H82138	probable phosphat
35	7	1.3	311	2 A57223	pheromone receptor
36	7	1.3	315	2 B86342	probable cdc2 kina
37	7	1.3	316	2 A55975	galectin-8 - rat
38	7	1.3	316	2 G64384	transketolase (EC
39	7	1.3	323	2 T44256	thiamin biosynthes
40	7	1.3	324	1 UC4985	UTP-glucose-1-phos
41	7	1.3	338	2 S78045	erythrocyte membra
42	7	1.3	338	2 T02645	hypothetical prote
43	7	1.3	342	2 D86677	transcription regu
44	7	1.3	363	2 S31780	peroxidase (EC 1.1
45	7	1.3	376	2 C69813	RNA helicase homol
46	7	1.3	383	2 G84248	iron-binding prote
47	7	1.3	390	2 H83856	chorismate synthas
48	7	1.3	391	2 T32156	hypothetical prote
49	7	1.3	396	2 G71044	probable molybdopt
50	7	1.3	400	1 URX1A1	peptidylglycine mo
51	7	1.3	400	2 F75275	chromate transport
52	7	1.3	427	2 C83464	hypothetical prote
53	7	1.3	429	2 D78468	conserved hypotnet
54	7	1.3	433	2 H84826	hypothetical prote
55	7	1.3	436	2 H87329	conserved hypotnet
56	7	1.3	438	2 G96945	similar to ABC tra
57	7	1.3	446	2 S67437	Damage and replica
58	7	1.3	452	1 GMEBT	indole-3-glycerol
59	7	1.3	452	1 AD0653	hypothetical prote
60	7	1.3	455	2 S80725	hypothetical prote
61	7	1.3	456	2 C86624	hypothetical prote
62	7	1.3	456	2 H72000	hypothetical prote
63	7	1.3	457	2 H84716	hypothetical prote
64	7	1.3	458	2 T31237	trab protein homol
65	7	1.3	468	2 AB0423	probable outer mem
66	7	1.3	495	2 S43294	bone morphogenetic
67	7	1.3	496	2 C85789	hypothetical prote
68	7	1.3	501	2 UC2347	growth/differentia
69	7	1.3	501	2 A55452	cartilage-derived
70	7	1.3	529	2 T20121	hypothetical prote
71	7	1.3	535	2 S74703	hypothetical prote
72	7	1.3	540	2 T48074	hypothetical prote
73	7	1.3	547	2 C66264	protein F319.5 [i
74	7	1.3	556	2 B84939	hypothetical prote
75	7	1.3	556	2 G90940	hypothetical prote
76	7	1.3	563	2 T04598	hypothetical prote
77	7	1.3	579	2 F83946	pyruvate synthase
78	7	1.3	585	1 A41292	glutamate decarbox
79	7	1.3	585	1 S38533	glutamate decarbox
80	7	1.3	585	1 JC0064	glutamate decarbox
81	7	1.3	594	2 B88956	protein ZK697.5 [i
82	7	1.3	594	2 F81113	protein ZK742.2 [i
83	7	1.3	602	1 S38111	amino acid transpo
84	7	1.3	606	2 S13526	hydrogenase (EC 1.
85	7	1.3	610	2 S56643	hydrogenase (EC 1.
86	7	1.3	613	2 S19676	68k protein - phag
87	7	1.3	617	2 F83744	ferrous iron trans
88	7	1.3	620	2 A85504	hypothetical prote
89	7	1.3	670	2 A12223	transketolase (imp
90	7	1.3	681	2 F85062	hypothetical prote
91	7	1.3	684	2 S60266	novel antigen rece
92	7	1.3	733	2 C66258	protein F5011.8 [i
93	7	1.3	736	1 VPXRPC	outer layer protei
94	7	1.3	751	2 A54053	amine oxidase (cop
95	7	1.3	758	2 D71072	hypothetical prote
96	7	1.3	839	2 H97758	outer membrane ass
97	7	1.3	878	2 T08559	protein kinase hom
98	7	1.3	910	2 T44477	hypothetical prote
99	7	1.3	985	2 S54485	hypothetical prote
100	7	1.3	935	2 S17855	peptidylglycine mo

ALIGNMENTS

RESULT 1

121616

hypothetical protein F32A11.3 - *Caenorhabditis elegans*C/Species: *Caenorhabditis elegans*

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: J21616

R/Type, R.

submitted to the EMBL Data Library, November 1996

A/Reference number: 219450

A/Accession: J21616

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-553 <WILL>

A/Cross-references: UNIPROT:O62197; EMBL:Z81521; PTDN:CAB04225.1; GSPDB:GN00020; CESP:F3

A/Experimental source: clone F32A11

C/Genetics:

A/Gene: CESP:F32A11.3

A/Map position: 2

A/Introns: 21/1; 221/3; 298/3

Query Match 1.5%; Score 8; DB 2; Length 353;
 Best Local Similarity 100.0%; Pred. No. 8.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 350 RSVLSLSA 357
 |||||
 DB 53 RSVLSLSA 60

RESULT 2

B84648

hypothetical protein At2g25420 [imported] - *Arabidopsis thaliana*C/Species: *Arabidopsis thaliana* (mouse-ear cress)

C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C/Accession: B84648

R/Lin. X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A/Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.

A/Reference number: A84420; MUID:20083487; PMID:10612197

A/Accession: B84648

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-572 <STO>

A/Cross-references: UNIPROT:Q9SKK7; GB:AEO02093; NID:g4432854; PTDN:AAD20702.1; GSPDB:GN

C/Genetics:

A/Gene: At2g25420

A/Map position: 2

Query Match 1.5%; Score 8; DB 2; Length 572;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 DILCITLQ 79
 |||||
 DB 96 DILCITLQ 103

RESULT 3

S22221

peroxidase (EC 1.11.1.7) - imperfect fungus (*Archiomyces ramosus*) (fragment)C/Species: *Archiomyces ramosus*

C/Date: 12-Feb-1998 #sequence_revision 17-Apr-1998 #text_change 12-Jul-2004

C/Accession: S22221

R/Kjalke, M.; Andersen, M.B.; Schneider, P.; Christensen, B.; Schuelein, M.; Welinder, K.

Biochim. Biophys. Acta 1120, 248-256, 1992

A/Title: Comparison of structure and activities of peroxidases from *Coprinus cinereus*, C

A/Reference number: S21746; MUID:92247803; PMID:1576150

A/Accession: S22221

A/Molecule type: protein
 A/Residues: 1-25 <KJA>
 C/Superfamily: Peroxidase
 C/Keywords: blocked amino end; glycoprotein; oxidoreductase

Query Match 1.3%; Score 7; DB 2; Length 25;
 Best Local Similarity 100.0%; Pred. No. 8.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 463 SLIPPG 469
 |||||
 DB 10 SLIPPG 16

RESULT 4

S76012

hypothetical protein - *Synechocystis* sp. (strain PCC 6803)C/Species: *Synechocystis* sp.

A/Variety: PCC 6803

C/Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C/Accession: S76012

R/Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda,

DNA Res. 3, 109-136, 1996

A/Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*

S.

A/Reference number: S74322; MUID:97061201; PMID:8905231

A/Accession: S76012

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-84 <KAN>

A/Cross-references: UNIPROT:P74781; EMBL:D64006; GB:AB001339; NID:g1001291; PTDN:BA10855

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C/Superfamily: conserved hypothetical protein H10721

Query Match 1.3%; Score 7; DB 2; Length 84;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 QVPHSL 184
 |||||
 DB 49 QVPHSL 55

RESULT 5

E86163

protein F15K9.18 [imported] - *Arabidopsis thaliana*C/Species: *Arabidopsis thaliana* (mouse-ear cress)

C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C/Accession: E86163

R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizart, L.

Nature 408, 816-820, 2000

A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.

ker, M.; Wu, D.; Xu, G.; Fraser, C.M.; Venter, C.J.; Davis, R.W.

A/Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.

A/Reference number: A86141; MUID:21016719; PMID:11130712

A/Accession: E86163

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-91 <STO>

A/Cross-references: UNIPROT:Q9ZVS3; GB:AF005172; NID:g3850586; PTDN:AACT2126.1; GSPDB:GN

C/Genetics:

A/Gene: F15K9.18

A/Map position: 1

Query Match 1.3%; Score 7; DB 2; Length 91;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 LIAFTRO 322
 |||||
 DB 80 LIAFTRO 86

RESULT 6

B75134
 hypothetical protein PAB7218 - *Pyrococcus abyssi* (strain Orsay)
 C/Species: *Pyrococcus abyssi*
 C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
 C/Accession: B75134
 R/anonymous, Genoscope
 submitted to the EMBL Data Library, July 1999
 A/Description: *Pyrococcus abyssi* genome sequence: insights into archaeal chromosome stru
 A/Reference number: A75001
 A/Accession: B75134
 A/Status: Preliminary
 A/Molecule type: DNA
 A/Residues: 1-96 <KMW>
 A/Cross-references: UNIPROT:Q9V0B7; GB:AJ248285; GB:AL096836; NID:95458067; PIDN:CAB4978
 A/Experimental source: strain Orsay
 C/Genetics:
 A/Gene: PAB7218

Query Match 1.3%; Score 7; DB 2; Length 96;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 196 NDALIVL 202
 |||||
 DB 63 NDALIVL 69

RESULT 7

B55863
 excisionase - *Streptococcus pneumoniae* transposon Tns252
 C/Species: *Streptococcus pneumoniae*
 C/Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
 C/Accession: B55863
 R/Kilic, A.O.; Vijayakumar, M.N.; Al-Khalidi, S.F.
 J. Bacteriol. 176, 5145-5150, 1994
 A/Title: Identification and nucleotide sequence analysis of a transfer-related region in
 A/Reference number: A55863; MUID:94327488; PMID:8051031
 A/Accession: B55863
 A/Status: Preliminary
 A/Molecule type: DNA
 A/Residues: 1-110 <KIL>
 A/Cross-references: UNIPROT:Q54878; GB:U29324; NID:94063727; PIDN:AAC98429.1; PID:946002
 C/Superfamily: *Streptococcus pneumoniae* transposon Tns252 excisionase

Query Match 1.3%; Score 7; DB 2; Length 110;
 Best Local Similarity 100.0%; Pred. No. 34;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 YKDPITG 58
 |||||
 DB 21 YKDPITG 27

RESULT 8

AH0243
 4-carboxymuconolactone decarboxylase (EC 4.1.1.44) [Imported] - *Yersinia pestis* (strain
 C/Species: *Yersinia pestis*
 C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
 C/Accession: AH0243
 R/Parikhilli, J.; Wren, B.W.; Thomson, N.R.; Tilball, R.W.; Holden, M.T.G.; Pentice, M.B.
 deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett,
 Nature 413, 523-527, 2001
 A/Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
 A/Reference number: AB0001; MUID:21470413; PMID:11586360
 A/Accession: AH0243

A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-140 <KUR>
 A/Cross-references: UNIPROT:Q8ZBZ7; GB:AL590842; PIDN:CAC90812.1; PID:915980013; GSPDB:GT
 C/Genetics:
 A/Gene: YPO1999
 C/Keywords: carbon-carbon lyase; carboxy-lyase

Query Match 1.3%; Score 7; DB 2; Length 140;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 LRSRLRL 32
 |||||
 DB 92 LRSRLRL 98

RESULT 9

S73394
 hypothetical protein R02_crlf50 - *Mycoplasma pneumoniae* (strain ATCC 29342)
 C/Species: *Mycoplasma pneumoniae*
 A/Variety: ATCC 29342
 C/Date: 26-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
 C/Accession: S73394
 R/Himmelreich, R.; Hilbert, H.; Plagens, H.; Pitkl, E.; Li, B.C.; Herrmann, R.
 Nucleic Acids Res. 24, 4420-4449, 1996
 A/Title: Complete sequence analysis of the genome of the bacterium *Mycoplasma pneumoniae*.
 A/Reference number: S73327; MUID:97105885; PMID:8948633
 A/Accession: S73394
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-150 <HLV>
 A/Cross-references: UNIPROT:P75606; EMBL:AE000009; GB:U00089; NID:91673720; PIDN:AAB95714
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
 C/Genetics:
 A/genetic code: SGC3

Query Match 1.3%; Score 7; DB 2; Length 150;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 328 DVFGLV 334
 |||||
 DB 94 DVFGLV 100

RESULT 10

AEAIAC
 allophycocyanin alpha chain - *Anabaena cylindrica*
 C/Species: *Anabaena cylindrica*
 C/Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
 C/Accession: A24224
 R/Mimami, Y.; Yamada, F.; Hase, T.; Matsubara, H.; Murakami, A.; Fujita, Y.; Takao, T.; S
 FEBS Lett. 191, 216-220, 1985
 A/Title: Amino acid sequences of allophycocyanin alpha- and beta-subunits isolated from
 A/Reference number: A91349
 A/Accession: A24224
 A/Molecule type: protein
 A/Residues: 1-160 <MIN>
 A/Cross-references: UNIPROT:P07325
 C/Comment: This protein is a common component of light-gathering protein complexes called
 C/Superfamily: phycocyanin
 C/Keywords: chromoprotein; photosynthesis; phycocyanobilin
 F/80/Binding site: phycocyanobilin (Cys) (covalent) #status experimental

Query Match 1.3%; Score 7; DB 1; Length 160;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 YGIVSGD 72
 |||||
 DB 93 YGIVSGD 99

RESULT 11
A13185
aliphycocyanin alpha-1 chain - Calothrix sp. (PCC 7601)
C/Species: Calothrix sp.
C/Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 11-Jun-1999
C/Accession: A13185; A30764
R/Houmard, J.; Capuano, V.; Coursin, T.; Tandeau de Marsac, N.
J. Bacteriol. 170..5512-5521, 1988
A/Title: Genes encoding core components of the phycobiosome in the cyanobacterium Calot
A/Reference number: A31890; MUID:85053869; PMID:24613358
A/Accession: A13185
A/Molecule type: DNA
A/Residues: 1-161 <HOU>
A/Cross-references: GB:M20806; NID:G148538; PIDN:AAA24874.1; PID:G148540
C/Superfamily: phycocyanin
C/Keywords: chromoprotein; photosynthesis; phycocyanobilin
F/81/Binding site: phycocyanobilin (Cys) (covalent) #status predicted

Query Match 1.3%; Score 7; DB 2; Length 161;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 YGIVSGD 72
DB 94 YGIVSGD 100

RESULT 12
F97162
hypothetical protein CAC2131 [imported] - Clostridium acetobutylicum
C/Species: Clostridium acetobutylicum
C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C/Accession: F97162
R/Nolling, J.; Breton, G.; Koeck, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.
J. Bacteriol. 183. 4823-4838, 2001
J. Dally, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A/Reference number: A96900; MUID:21359325; PMID:21539325
A/Accession: F97162
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-167 <KTR>
A/Cross-references: UNIPROT:Q97H82; GB:AE001437; PIDN:AAK60089.1; PID:G15025122; GSPDB:G
A/Experimental source: Clostridium acetobutylicum ATCC824
C/Genetics: A;Gene: CAC2131

Query Match 1.3%; Score 7; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 339 LKRIFR 345
DB 103 LKRIFR 109

RESULT 13
AG1489
hypothetical protein lin0455 [imported] - Listeria innocua (strain C11P11262)
C/Species: Listeria innocua
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C/Accession: AG1489
R/Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Feihl, H.
D.; Jones, L.M.; Kars, U.
Science 294. 849-852, 2001
A/Authors: Kretz, U.; Kunz, M.; Kunst, F.; Kurapkac, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tiller, A.; Vazquez-Belard, J.A.; Voss, H.; Wehland, A.
A/Title: Comparative genomics of Listeria species.
A/Reference number: AB1077; MUID:21537279; PMID:11679669
A/Accession: AG1489
A/Status: preliminary

A/Molecule type: DNA
A/Residues: 1-184 <GLA>
A/Cross-references: UNIPROT:Q92EK4; GB:AL592022; PIDN:CAC95687.1; PID:G16412896; GSPDB:G
A/Experimental source: strain C11P11262
C/Genetics: A;Gene: lin0455

Query Match 1.3%; Score 7; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 333 VVLPLEL 339
DB 59 VVLPLEL 65

RESULT 14
T26741
hypothetical protein Y39A1A.21 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T26741
R/Wall, M.
submitted to the EMBL Data Library, September 1998
A/Reference number: Z20257
A/Accession: T26741
A/Status: preliminary; translated from GB/EMBL/DBD
A/Molecule type: DNA
A/Residues: 1-188 <WIL>
A/Cross-references: UNIPROT:Q9XX11; EMBL:AL031633; PIDN:CAA21030.1; GSPDB:GN00021; CESP:Y
A/Experimental source: clone Y39A1A
C/Genetics: A;Gene: CBSP:Y39A1A.21
A/Map position: 3
A/Intons: 76/3; 114/2; 171/3

Query Match 1.3%; Score 7; DB 2; Length 188;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 SLATSSN 111
DB 53 SLATSSN 59

RESULT 15
B87271
general secretion pathway protein J [imported] - Caulobacter crescentus
C/Species: Caulobacter crescentus
C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C/Accession: B87271
R/Nietman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Neilson, K.E.; Eisen, J.; Heidelberg, J.;
B.; Lamb, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolome
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98. 4136-4141, 2001
A/Title: Complete genome sequence of Caulobacter crescentus.
A/Reference number: AB7249; MUID:21173698; PMID:11259647
A/Accession: B87271
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-196 <STO>
A/Cross-references: UNIPROT:Q9ABP7; GB:AE005673; NID:G13421298; PIDN:AAK22166.1; GSPDB:G
A/Genetics: A;Gene: CC0179
C/Superfamily: secretion protein xcpW

Query Match 1.3%; Score 7; DB 2; Length 196;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 315 PULAFTR 321
DB 89 PULAFTR 95

RESULT 16
AF2026
hypothetical protein all1764 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AF2026
R:Kanevo, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Matanabe, A.; Iriyuchi, Nakazaki, N.; Shimp, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 9, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AF2026
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-216 <KUR>
A:Cross-references: UNIPROT:Q8YWE2; GB:BA000019; PIDD:BA73463.1; PID:G17130854; GSPDB:C
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all1764

Query Match 1.3%; Score 7; DB 2; Length 216;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 122 DSFOGQA 128
Db 103 DSFOGQA 109

RESULT 17
G72398
hypothetical protein TM0246 - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: G72398
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: G72398
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-224 <ARN>
A:Cross-references: UNIPROT:Q9WY88; GB:AE001708; GB:AE000512; NID:G4980740; PIDD:AAD3533
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM0246
C:Superfamily: Thermotoga maritima hypothetical protein TM0246

Query Match 1.3%; Score 7; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 KDPLTGD 59
Db 50 KDPLTGD 56

RESULT 18
AH0875
probable membrane protein SRY331 [imported] - Salmonella enterica subsp. enterica serov
C:Species: Salmonella enterica subsp. enterica serovar Typh
A:Note: this species has also been called Salmonella typh
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AH0875
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher, th, T.; Comercon, P.; Goun, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moutle, S.; O'Gaora, P.

Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AH0875
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-224 <PAR>
A:Cross-references: GB:AL513382; PIDD:CAD02904.1; PID:G16504157; GSPDB:GN00176
C:Genetics:
A:Gene: SRY331

Query Match 1.3%; Score 7; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 437 SRLPPI 443
Db 108 SRLPPI 114

RESULT 19
F70800
probable transport system permease protein - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: F70800
R:Cole, S.T.; Broesch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrett, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295587; PMID:9634230
A:Accession: F70800
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-229 <COL>
A:Cross-references: UNIPROT:O69723; GB:AL022121; GB:AL123456; NID:G3261559; PIDD:CAA1807
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: p708
C:Superfamily: ABC transporter permease protein

Query Match 1.3%; Score 7; DB 2; Length 229;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 HRLSL 35
Db 18 HRLSL 24

RESULT 20
T04166
chaumatin-like protein - rice
C:Species: Oryza sativa (rice)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T04166
R:Cole, K.C.; Velazhathan, R.; Anuratha, C.S.; Muthukrishnan, S.
submitted to the EMBL Data Library, November 1996
A:Description: Induction of chaumatin-like proteins (TLPs) in Rhizoctonia solani - infecte
A:Reference number: Z15250
A:Accession: T04166
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-238 <COL>
A:Cross-references: UNIPROT:O04364; EMBL:U77657; NID:G2062388; PIDD:AA53368.1; PID:G206;
C:Superfamily: chaumatin I

Query Match 1.3%; Score 7; DB 2; Length 238;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	104	PSLATSS	110
Db	10	PSLATSS	16

RESULT 21

D81804
 Hypotheetical protein NMA1789 [imported] - Neisseria meningitidis (strain Z2491 serogroup
 C) [Species: Neisseria meningitidis
 C] [Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
 C] [Accession: D81804
 E; Parkhill, J., Achtman, M., James, K.D., Bentley, S.D., Churcher, C., Klee, S.R., Morel
 E; Holtroyd, S., Jagsels, K., Leather, S., Moule, S., Mungall, K., Quail, M.A., Rajandream,
 Nature 404, 502-506, 2000
 A] [Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
 A] [Reference number: A81775; MUID:20222556; PMID:10761919
 A] [Accession: D81804
 A] [Status: preliminary
 A] [Molecule type: DNA
 A] [Residues: 1-243 #PAR>
 A] [Cross-references: UNIPROT:Q9UTG3; GB:A1162157; GB:A1157959; NID:5738037; PIDN:CAH8501
 A] [Experimental source: serogroup A, strain Z2491
 C] [Genetics:
 A] [Gene: NMA1789
 C] [Superfamily: Neisseria meningitidis hypotheetical protein NMA1789

```
Query Match      1.3%  Score 7;  DB 2;  Length 243;
Best Local Similarity 100.0%  Pred. No. 68;
Matches 7;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
```

QY	332	LVLPLE	338
Db	200	LVLPLE	206

RESULT 22

T16371
hypothetical protein F45E12.1 - *Caenorhabditis elegans*
C/Species: *Caenorhabditis elegans*
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T16371
R/Lattreille, P
submitted to the EMBL Data Library, June 1995
A/Description: The sequence of C. elegans cosmid F45E12.
A/Reference number: Z18501
A/Accession: T16371
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-246 <LAT>
A/Cross-references: UNIPROT:Q02432; EMBL:U29536; NID:G868261; PIDN:G868266; PIDN:AA68794
A/Experimental source: strain Bristol N2
C/Genetics:
A/Gene: CBSP:F45E12.1
A/Introns: 29/3; 53/1; 92/3; 120/2; 151/2; 193/1

```

Query Match      1.3%   Score 7;  DB 2;
Best Local Similarity 100.0%   Pred. No. 69;
Matches 7;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

```

QY	348	DVRSVLS	354
Dib	225	DVRSVLS	231

RESULT 23

A96033 Probable thiamine biosynthesis protein [imported] - *Sinorhizobium meliloti* (strain 1021)
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C:Accession: A96033
R:Rifan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vornholter, F.J.; Hernat
Proc. Natl. Acad. Sci. U.S.A. 98, 9885-9894, 2001

A>Title: The complete sequence of the 1,683-kb pSYM5 megaplasmid from the N2-fixing endo-
A,Reference number: A95842; MUID:21396508; PMID:11491431
A,Accession: A96033
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-657 <KUF>

A:Cross-references: UNIPROT:P58264; G3:AL551985; PIDN:G15144147; GSPDB:Q1A:Experimental source: strain 1021, megasalmodi p58m
R:Galibert, F.; Flamin, T.M.; Long, S.R.; Philier, A.; Abola, P.; Ampe, F.; Barlier-Hubier, P.; Chalm, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Fethergill, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kaiman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, M.; Neuhart, P.; Vandenbol, M.; Vorholter, F.U.; Weidner, S.; Wells, D.H.; Wong, K.; Yen, K.
A:Title: The complete genome of the euglenid symbiont *Sinorhizobium meliloti*.
A:Reference number: A56035; MUID:21568234; PMID:11474104
A:Contents: annotation

Query Match	1.3%	Score 7;	DB 2;	length 257;
Best Local Similarity	100.0%	Pred. No. 72;		
Matches	7;	Conservative 0;	Mismatches 0;	Indels 0;

QY	327	PDVFGLV	333
Db	108	PDVFGLV	114

RESULT 24

A60404
 MHC class II histocompatibility antigen SLA-DQ-c beta chain precursor - pig
 C/Species: Sus scrofa domestica (domestic pig)
 C/Date: 08-Dec-1992 #sequence_revison 08-Dec-1992 #ext_change 09-Jul-2004
 C/Accession: A60404
 R/Gustafsson, K., Leguenn, C., Hirsch, F., Gemma, S., Prati, K., Sachs, D.H.
 J. Immunol. 145, 1946-1951, 1990
 A>Title: Class II genes of miniature swine. Characterization and expression of two alleles
 A/Reference number: A60404; MUID:90361905; PMID:2391424
 A/Accession: A60404
 A/Status: not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-261 <UNSP>
 A/Cross-references: UNIPROT: P15982; GB:M32117; NID:9164577; PIDN:AAA5110.1; PID:9164578
 C/Superfamily: class II histocompatibility antigen; immunoglobulin homology
 C/Keywords: transmembrane protein #status predicted <SITE>
 F1-32/Domains: signal sequence #status predicted <SITE>
 F13-261/Product: MHC class II histocompatibility antigen SLA-DQ-c beta chain #status predicted
 F142-207/Domains: immunoglobulin homology <IM>

```

Query Match      1.3%;   Score 7; DB 2;   Length 251;
Best Local Similarity 100.0%;   Pred. No. 73;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY	94	EHSSLQN	100
Db	208	EHSSLQN	214

RESULT 25

F69541
spermidine synthase (speE) homolog - Archaeoglobus fulgidus
C/Species: Archaeoglobus fulgidus
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #ext_change 09-Jul-2004
C/Accession: F69541
R/Klink, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, J.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kiriwense, E.F.; Glock, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 366-370, 1997
A/Authors: Overbeek, T.; Connor, M.D.; Spriggs, T.; Artach, P.; Kaine, B.P.; Sykes, S.L.; Smith, H.O.; Woese, C.R.; Venter, J.C.

Nature 390, 364-370, 1997
 A: Authors: Uterback, T.; Cotton, M.D.; Spilgins, T.; Attiach, P.; Kaine, B.P.; Sykes, S.
 Smith, H.O.; Moese, C.R.; Venter, J.C.

A>Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae
A/Reference number: A69250; MIMD:9809343; PMID:9389475
A/Accession: F69541
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-269 <XLE>
A/Cross-references: UNIPROT:Q27950; GB:AE000943; GB:AE000782; NID:G2689266; PIDN:AA8891
C/Superfamily: spermidine synthase

Query Match 1.3%; Score 7; DB 2; Length 269;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 443 IIGGEYD 449
DB 222 IIGGEYD 228

RESULT 26
D84312
sulfate transport system permease protein [imported] - Halobacterium sp. NRC-1
C/Species: Halobacterium sp. NRC-1
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C/Accession: D84312
R/NG: W.V.; Kennedy, S.P.; Maharez, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Jaeky, S.;
Leithausen, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jaldic
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A/Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A/Title: Genome sequence of Halobacterium species NRC-1.
A/Reference number: A84160; MIMD:20504483; PMID:11016950
A/Accession: D84312
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-269 <SNO>
A/Cross-references: UNIPROT:Q9HFK3; GB:AE004437; NID:G10581074; PIDN:AA319864.1; GSPDB:C
C/Genetics:
A/Gene: cyst2
C/Superfamily: maltose transport protein malG

Query Match 1.3%; Score 7; DB 2; Length 269;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 331 GLVVLPL 337
DB 95 GLVVLPL 101

RESULT 27
T31506
hypothetical protein Y116A8C.40 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C/Accession: T31506
R/McMurray, A.
submitted to the EMBL Data Library, October 1999
A/Reference number: Z21041
A/Accession: T31506
A/Status: preliminary; translated from GB/EMBL/DD347
A/Molecule type: DNA
A/Residues: 1-273 <WIL>
A/Cross-references: UNIPROT:Q9J2T7; EMBL:AL117204; PIDN:CAB55140.1; CESP:Y116A8C.40
A/Experimental source: clone Y116A8C
A/Genetics:
A/Gene: CESP:Y116A8C.40
A/Introns: 38/2; 83/2; 130/3; 236/1

Query Match 1.3%; Score 7; DB 2; Length 273;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 351 SVLSLSA 357

DB 9 SVLSLSA 15

RESULT 28
B99415
hypothetical protein cutB-1 [imported] - Sulfolobus solfataricus
C/Species: Sulfolobus solfataricus
C/Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
R/She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aways, M.J.; Chan-V
Jong, I.; Jeffries, A.C.; Kozera, C.D.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
arrest, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A/Description: Sulfolobus solfataricus complete genome.
A/Reference number: A89139
A/Accession: B99415
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-278 <XUR>
A/Cross-references: UNIPROT:Q97W13; GB:AE006641; NID:G13815737; PIDN:AAK42577.1; GSPDB:C
C/Genetics:
A/Gene: cutB-1
C/Superfamily: carbon monoxide dehydrogenase medium chain

Query Match 1.3%; Score 7; DB 2; Length 278;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 339 LKLRIFR 345
DB 40 LKLRIFR 46

RESULT 29
S78602
peroxidase (EC 1.11.1.7) - inky cap (Coprinus macrohizus) (fragments)
C/Species: Coprinus macrohizus
C/Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 12-Jul-2004
C/Accession: S78602; S22220
R/Baunsgaard, L.; Dalboe, H.; Houen, G.; Rasmussen, E.M.; Wellinder, K.G.
Eur. J. Biochem. 213, 605-611, 1993
A/Title: Amino acid sequence of Coprinus macrohizus peroxidase and cDNA sequence encodir
A/Reference number: S30357; MIMD:93238741; PMID:8477731
A/Accession: S78602
A/Molecule type: protein
A/Residues: 1-17;18-27;28-59;60-138;139-141;142-256;257-281;282-287;288-291 <BAU>
R/Kjaikje, M.; Andersen, M.B.; Schneider, P.; Christensen, B.; Schneider, M.; Wellinder, K.
Biochim. Biophys. Acta 1120, 248-256, 1992
A/Title: Comparison of structure and activities of peroxidases from Coprinus cinereus, C
A/Reference number: S21746; MIMD:92247803; PMID:1576150
A/Accession: S22220
A/Molecule type: protein
A/Residues: 97-121 <XJA>
C/Superfamily: peroxidase
C/Keywords: blocked amino end; glycoprotein; oxidoreductase; pyroglyutamic acid
F/Modified site: pyroliodone carboxylic acid (Gln) #status experimental

Query Match 1.3%; Score 7; DB 2; Length 291;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 463 SLIRPGG 469
DB 106 SLIRPGG 112

RESULT 30
A47125
transcription activator of cholera toxin toxR - Vibrio parahaemolyticus (strain A03815)
C/Species: Vibrio parahaemolyticus
C/Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C/Accession: A47125

R, Lin, Z.; Kumagai, K.; Baba, K.; Mekalanos, J.J.; Nishibuchi, M.
J. Bacteriol. 175, 3844-3855, 1993
A:Title: Vibrio parahaemolyticus has a homolog of the Vibrio cholerae toxS operon that
A:Reference number: A47125; MUID:93285998; PMID:8509337
A:Accession: A47125
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-292 <LIN>
A:Cross-references: UNIPROT:Q05938; GB:L11929; NID:g295440; PIDN:AAA27576.1; PID:g295441
A:Note: authors translated the codon AGC for residue 28 as Thr
C:Genetics:
A:Gene: toxR
C:Keywords: DNA binding; transcription regulation; transmembrane protein

Query Match 1.3%; Score 7; DB 2; Length 292;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 104 PSLATSS 110
DB 147 PSLATSS 153

RESULT 31
B95939
Probable spermidine/putrescine ABC transporter permease protein potB [imported] - Sinorhizobium meliloti
C:Species: Sinorhizobium meliloti
C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C:Accession: B95939
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhmester, J.; Chain, P.; Vorholter, F.J.; Hernan Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A:Title: The complete sequence of the 1.683-kb P5YMB megaplasmid from the N2-fixing endo A:Reference number: A95842; MUID:21396508; PMID:11481431
A:Accession: B95939
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-299 <KTR>
A:Cross-references: UNIPROT:Q92VD0; GB:AL591985; PIDN:CAC49178.1; PID:g1514063; GSPDB:Q R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, P.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, heault, P.; Vandenberg, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: potB; SMD21274
A:Genome: plasmid
C:Superfamily: spermidine/putrescine transport system permease protein potB

Query Match 1.3%; Score 7; DB 2; Length 299;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 331 GLVVLPL 337
DB 121 GLVVLPL 127

RESULT 32
C72324
homoserine O-succinyltransferase - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: C72324
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garret, M.W.; Stewart, A.W.; Cotton, M.D.; Pratt, W.S.; Phillips, C.A.; Richardson, D.; C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq

A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: C72324
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-304 <ARN>
A:Cross-references: UNIPROT:Q9WZY3; GB:AE001753; GB:AE000512; NID:g4981397; PIDN:AAD3596; C:Genetics:
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM0881
C:Superfamily: homoserine O-succinyltransferase

Query Match 1.3%; Score 7; DB 2; Length 304;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 229 KLSGVYK 235
DB 163 KLSGVYK 169

RESULT 33
A83123
probable transcription regulator PA4174 [imported] - Pseudomonas aeruginosa (strain PAO1)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: A83123
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Er adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Latif, K.; Lim, .; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathog A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: A83123
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-307 <STO>
A:Cross-references: UNIPROT:Q9HWK7; GB:AE004834; GB:AE004091; NID:g9950382; PIDN:AA07561 A:Experimental source: strain PAO1
C:Genetics:
A:Gene: PA4174

Query Match 1.3%; Score 7; DB 2; Length 307;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 RLVRLL 8
DB 43 RLVRLL 49

RESULT 34
H82138
Probable phosphatidate cytidyllyltransferase VC1936 [imported] - Vibrio cholerae (strain C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: H82138
R:Heideberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, P 1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: H82138
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-310 <HEI>
A:Cross-references: UNIPROT:Q9XOR2; GB:AE004269; GB:AE003852; NID:g9656466; PIDN:AAF5508; A:Experimental source: serogroup O1, strain N16961, biotype El Tor
C:Genetics:
A:Gene: VC1936
A:Map position: 1

Query Match 1.3%; Score 7; DB 2; Length 310;

Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 337 LEIKRI 343
DB 39 LEIKRI 45

RESULT 35

A57223

Pheromone receptor VN3 - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C/Accession: A57223

R/Dulac, C.; Axel, R.

Cell 83, 195-206, 1995

A/Title: A novel family of genes encoding putative pheromone receptors in mammals.

A/Reference number: A57223; MUID:96028094; PMID:7585937

A/Accession: A57223

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-311 <RES>

A/Cross-references: UNIPROT:Q62852; EMBL:U36895; NID:g1055247; PIND:AA652284.1; PID:g105

C/Superfamily: pheromone receptor VN3c

Query Match 1.3%; Score 7; DB 2; Length 311;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 202 LIHML 208
DB 58 LIHML 64

RESULT 36

B86342

Probable cdcc2 kinase (imported) - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C/Accession: B86342

R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chen, C.W.; Chung, M.K.; Com, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A/Reference number: A61411; MUID:21016719; PMID:11130712

A/Accession: B86342

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-315 <STO>

A/Cross-references: UNIPROT:Q98YPA; GB:AF005172; NID:g4836894; PIND:AA030597.1; GSPDB:GN

C/Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 1.3%; Score 7; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 341 LRIRRL 347
DB 234 LRIRRL 240

RESULT 37

A55975

Galectin-8 - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004

C/Accession: A55975

R/Hadadi, Y.R.; Paz, K.; Dekel, R.; Mestrovic, T.; Accilli, D.; Zick, Y.

J. Biol. Chem. 270, 3447-3453, 1995

A/Title: Galectin-8. A new rat lectin, related to galectin-4.

A/Reference number: A55975; MUID:95155445; PMID:7852431

A/Accession: A55975

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-316 <HAD>

A/Cross-references: UNIPROT:Q62665; GB:U09824; NID:g717031; PIND:AA66359.1; PID:g717032

C/Superfamily: lactose-binding lectin L-36

Query Match 1.3%; Score 7; DB 2; Length 316;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 RLIDYRS 351
DB 309 RLIDYRS 315

RESULT 38

G64384

transketolase (EC 2.2.1.1) - Methanococcus jannaschii

C/Species: Methanococcus jannaschii

C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 12-Jul-2004

C/Accession: G64384

R/Bull, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,

; Reich, C.I.; Overbeek, R.; Kirsch, E.F.; Weissbach, K.G.; Merrick, J.M.; Glöck, A.;

ison, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.

Science 273, 1058-1073, 1996

A/Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.

A/Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.

A/Reference number: A6300; MUID:96337999; PMID:8688087

A/Accession: G64384

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-316 <BU>

A/Cross-references: UNIPROT:Q58092; GB:U67515; GB:L77117; NID:g1591390; PIND:AA096674.1;

C/Genetics:

A/Map position: REV606237-605287

C/Superfamily: transketolase, C-terminal subunit

C/Keywords: transferase

Query Match 1.3%; Score 7; DB 2; Length 316;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 KLSGVYK 235
DB 3 KLSGVYK 9

RESULT 39

T44256

thiamin biosynthesis protein thig [similarity] - Rhizobium etli plasmid b

C/Species: Rhizobium etli

C/Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 24-Oct-2000

C/Accession: T44256

R/Miranda-Rios, J.; Moreira, C.; Taboada, H.; Davalos, A.; Encarnacion, S.; Mora, J.; Sobr

J. Bacteriol. 179, 6887-6893, 1997

A/Title: Expression of thiamin biosynthetic genes (thiCGB) and production of symbiotic t

A/Reference number: Z22737; MUID:98037482; PMID:9371431

A/Accession: T44256

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-323 <MIR>

A/Cross-references: EMBL:AF004408; NID:g2627325; PIND:AA645974.1; PID:g2627328

A/Experimental source: strain CE3

C/Genetics:

A/gene: thig

A/genome: plasmid b

C/Function: involved in the biosynthesis of the thiazole moiety of thiamin
 A/Description: thiamin biosynthesis protein thig
 C/Superfamily: thiamin biosynthesis protein thig

Query Match 1.3%; Score 7; DB 2; Length 323;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 327 PDVFGLV 333
 |||||
 Db 174 PDVFGLV 180

RESULT 40

UTP-glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) [validated] - Xanthomonas campestris
 N/Alternate names: udp-glucose pyrophosphorylase
 C/Species: Xanthomonas campestris
 C/Date: 15-Dec-1996 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004

A/Accession: U04985
 R/Mel, C.L.; Lin, N.T.; Weng, S.F.; Tseng, Y.H.
 Biochem. Biophys. Res. Commun. 226, 607-612, 1996
 A/Title: The gene encoding UDP-glucose pyrophosphorylase is required for the synthesis of
 A/Reference number: U04985; MUID:96428562; PMID:8831665
 A/Accession: U04985

A/Molecule type: DNA
 A/Residues: 1-324 <WEB>
 A/Cross-references: UNIPROT:P74969; GB:U65532; NID:G1628574; PIDN:AAB17376.1; PID:G16285
 C/Genetics:
 A/Map position: Xc17
 C/Function:
 A/Description: catalyzes the reaction of UTP and glucose-1-phosphate to form UDP-1-glucose
 C/Superfamily: Escherichia coli UTP-glucose-1-phosphate uridylyltransferase
 C/Keywords: nucleotidyltransferase

Query Match 1.3%; Score 7; DB 1; Length 324;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 64 ASYGIVS 70
 |||||
 Db 171 ASYGIVS 177

RESULT 41

erythrocyte membrane-associated antigen (clone pPF 64) - Plasmodium falciparum (fragment
 C/Species: Plasmodium falciparum
 C/Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

A/Accession: S78045; S23690
 R/Kun, J.; Hesselbach, J.; Scherf, M.; Scherf, A.; Gysin, J.; Mattei, D.; Pereira da
 Res. Immunol. 142, 199-210, 1991
 A/Title: Cloning and expression of genomic DNA sequences coding for putative erythrocyte
 A/Reference number: S23684; MUID:91376328; PMID:1896607
 A/Accession: S78045

A/Status: nucleic acid sequence not shown; not compared with conceptual translation
 A/Molecule type: DNA
 A/Residues: 1-338 <KUN>
 A/Cross-references: UNIPROT:Q06166

R/Kun, J.
 submitted to the EMBL Data Library, May 1990
 A/Reference number: S23690

A/Accession: S23690
 A/Molecule type: DNA
 A/Residues: 1-104 <KUN>
 A/Cross-references: EMBL:X53021
 C/Superfamily: ring-infected erythrocyte surface antigen, draf amino-terminal homology
 C/Keywords: surface antigen

Query Match 1.3%; Score 7; DB 2; Length 338;
 Best Local Similarity 100.0%; Pred. No. 92;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 288 EXLGENV 294
 |||||
 Db 284 EXLGENV 290

RESULT 42

T02645
 hypothetical protein At2g26900 [imported] - Arabidopsis thaliana
 N/Alternate names: hypothetical protein F12C20.6
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004

A/Accession: T02645; C84666
 R/Rounsley, S.D.; Rounsley, C.M.; Lin, X.; Kechum, K.A.; Crosby, M.L.; Brandon, R.C.; Sy
 submitted to the EMBL Data Library, August 1998
 A/Description: Arabidopsis thaliana chromosome II BAC F12C20 genomic sequence.
 A/Reference number: T14685
 A/Accession: T02645

A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-338 <ROU>
 A/Cross-references: UNIPROT:O81017; EMBL:AC005168; NID:G3426033; PID:G3426051
 A/Experimental source: cultivar Columbia

R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.L.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.E.; Umayam, L.; Tallon, L.;
 euss, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
 Nature 402, 761-768, 1999
 A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A/Reference number: A84420; MUID:20083487; PMID:10617137
 A/Accession: C84666

A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-338 <STO>
 A/Cross-references: GB:AE002093; NID:G3426051; PIDN:AA032250.1; GSPDB:GN00139
 C/Genetics:
 A/Map position: 2
 A/Status: preliminary

A/Accession: F12C20.6
 A/Status: preliminary
 A/Map position: 2
 A/Status: preliminary

Query Match 1.3%; Score 7; DB 2; Length 338;
 Best Local Similarity 100.0%; Pred. No. 92;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 514 PTGRLS 520
 |||||
 Db 9 PTGRLS 15

RESULT 43

D86677
 transcription regulator [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
 C/Species: Lactococcus lactis subsp. lactis
 C/Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004

A/Accession: D86677
 R/Bolotin, A.; Winkler, P.; Mager, S.; Tallon, O.; Malarne, K.; Weissenbach, J.; Ehrlich
 Genome Res. 11, 731-753, 2001
 A/Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp
 A/Reference number: A86625; MUID:21235186; PMID:11337471
 A/Accession: D86677

A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-342 <STO>
 A/Cross-references: UNIPROT:Q9CIE3; GB:AE005176; PID:G127232395; PIDN:AA04518.1; GSPDB:GN
 A/Experimental source: strain IL1403
 C/Genetics:
 A/Status: preliminary

Query Match 1.3%; Score 7; DB 2; Length 342;
 Best Local Similarity 100.0%; Pred. No. 93;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 58 GDETLA 64
 |||||
 Db 314 GDETLA 320

RESULT 44

peroxidase (EC 1.11.1.7) precursor - inky cap (*Coprinus cinereus*)
 C/Species: *Coprinus cinereus*

C/Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #text_change 12-Jul-2004

C/Accession: S31780; S30357; S21746

R/Baarsgaard, L.; Wind, J.; Dalboge, H.
 submitted to the EMBL Data Library, January 1993

A/Reference number: S31780

A/Accession: S31780

A/Molecule type: DNA

A/Residues: 1-363 <BAU>

A/Cross-references: UNIPROT:Q12575; EMBL:X70789; NID:92538; PIDN:CAA50060.1; PID:92539

R/Baarsgaard, L.; Dalboge, H.; Hoven, G.; Rasmussen, E.M.; Welinder, K.G.

Eur. J. Biochem. 213, 605-611, 1993

A/Title: Amino acid sequence of *Coprinus macrohizus* peroxidase and cDNA sequence encoded

A/Reference number: S30357; MUID:93238741; PMID:8477731

A/Accession: S30357

A/Molecule type: mRNA

A/Residues: 1-118, 'V', 120-363 <BAU>

A/Cross-references: EMBL:X69457; NID:92540; PIDN:CAA49216.1; PID:92541

A/Experimental source: strain IFO 8371

R/Kjalke, M.; Andersen, M.B.; Schneider, P.; Christensen, B.; Schueler, M.; Welinder, K.

Biochim. Biophys. Acta 1120, 248-256, 1992

A/Title: Comparison of structure and activities of peroxidases from *Coprinus cinereus*, C

A/Reference number: S21746; MUID:92247803; PMID:1576150

A/Accession: S21746

A/Molecule type: protein

A/Residues: 161, 'X', 163-185 <KTA>

A/Experimental source: strain IFO 30114

C/Genetics:

A/Insertions: 41/3; 56/2; 63/1; 68/3; 71/3; 91/2; 96/1; 110/1; 136/2; 216/3; 234/3; 283/3;

C/Keywords: blocked amino end; glycoprotein; oxidoreductase; pyroglyutamic acid

F/1-20/Domain: signal sequence #status predicted <SIG>

F/21-363/Product: peroxidase #status predicted <MAY>

F/21/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experiment

F/162/Binding site: carboxylate (Asn) (covalent) #status predicted

F/351/Binding site: carboxylate (Thr) (covalent) #status predicted

F/358/Binding site: carboxylate (Ser) (covalent) #status predicted

Query Match

Best Local Similarity 1.3%; Score 7; DB 2; Length 363;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 170 SLIPPG 176

RESULT 45

RNA helicase homolog yfml - *Bacillus subtilis*

C/Species: *Bacillus subtilis*

C/Date: 05-Dec-1997 #sequence revision 05-Dec-1997 #text_change 09-Jul-2004

C/Accession: C69813

R/Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter

C./Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho

A./Enlrich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A/Authors: Foulger, D.; Filtz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall

tech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holzapfel, S.; Hosono, S.; Hullo, W.F.

Koetter, P.; Konigsmann, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Poh, T.M.; Portetelle

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon,

A/Authors: Schleich, S.; Schuster, R.; Scottone, F.; Sekiguchi, J.; Sekowska, A.; Seron

akerchi, M.; Tamaceni, A.; Tanaka, T.; Terpestra, P.; Tognoni, A.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wipet, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.

A/Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Zumbstein, E.

A/Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.

A/Reference number: A69580; MUID:98044033; PMID:9384377

A/Accession: C69813

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-376 <KUN>

A/Cross-references: UNIPROT:Q34750; GB:Z99108; GB:AL009126; NID:G2633055; PIDN:CA12572.1

A/Experimental source: strain 168

C/Genetics:

A/Supplementary: translation initiation factor eIF-4A

C/Keywords: ATP; nucleotide binding; P-loop

F/48-55/Region: nucleotide-binding motif A (P-loop)

F/153-156/Region: nucleotide-binding motif B

F/153-156/Region: DEAD motif

Query Match

Best Local Similarity 1.3%; Score 7; DB 2; Length 376;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 233 LOKLSRL 239

RESULT 46

iron-binding protein [imported] - *Halobacterium* sp. NRC-1

C/Species: *Halobacterium* sp. NRC-1

C/Date: 02-Feb-2001 #sequence revision 02-Feb-2001 #text_change 09-Jul-2004

C/Accession: G84248

R/Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.

; Leithausen, R.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor

Jung, K.H.; Alm, M.; Freilich, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A/Authors: Hou, S.; Daniels, C.O.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li

A/Title: Genome sequence of *Halobacterium* species NRC-1.

A/Reference number: A84160; MUID:20504483; PMID:11016950

A/Accession: G84248

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-383 <STO>

A/Cross-references: UNIPROT:Q9HR04; GB:AE004437; NID:G10580483; PIDN:AA619355.1; GSPDB:G

C/Genetics:

A/Genes: hbp

Query Match

Best Local Similarity 1.3%; Score 7; DB 2; Length 383;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 345 DEVGRLP 351

RESULT 47

chorismate synthase aroF [imported] - *Bacillus halodurans* (strain C-125)

C/Species: *Bacillus halodurans*

C/Date: 01-Dec-2000 #sequence revision 01-Dec-2000 #text_change 09-Jul-2004

C/Accession: H83856

R/Takami, H.; Nakase, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hirai

Nucleic Acids Res. 28, 4317-4331, 2000

A/Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and c

A/Reference number: A83850; MUID:20515582; PMID:11058132

A/Accession: H83856

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-390 <STO>

A/Cross-references: UNIPROT:Q9KCB7; GB:AP001512; GB:BA000004; NID:G10174030; PIDN:BA053

A/Experimental source: strain C-125

C/Genetics:

A/Genes: aroF

C:Superfamily: chorismate synthase

Query Match 1.3%; Score 7; DB 2; Length 390;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 PLTGDDE 61
|||
Db 92 PLTGDDE 98

RESULT 48

T32156
hypothetical protein C29G2.5 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C:Accession: T32156

R:Beck, C.; Wamsley, P.
submitted to the EMBL Data Library, September 1997

A:Description: The sequence of C. elegans cosmid C29G2.

A:Reference number: Z21128

A:Accession: T32156

A:Status: preliminary; translated from GB/EMBL/DDB

A:Molecule type: DNA

A:Residues: 1-391 <BEC>

A:Cross-references: UNIPROT:O16884; EMBL:AF022969; PDB:AA69894.1; GSPDB:GN00023; CESP:

A:Experimental source: strain Bristol N2; clone C29G2

A:Gene: CESP:C29G2.5

A:Map position: 5

A:introns: 8/1; 84/1; 113/1; 153/3; 175/3; 316/3

Query Match 1.3%; Score 7; DB 2; Length 391;
Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 461 ISSLIPG 467
|||
Db 211 ISSLIPG 217

RESULT 49

G71044

probable molybdoperoxin biosynthesis moeA protein - *Pyrococcus horikoshii*

C:Species: *Pyrococcus horikoshii*

C>Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004

C:Accession: G71044

R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki, M.; Ohnuki, Y.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kushida, N.; Oguchi, DNA Res. 5, 55-76, 1998

A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a

A:Reference number: A71000; MUID:98344137; PMID:9679194

A:Accession: G71044

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-396 <KAN>

A:Cross-references: UNIPROT:O59354; GB:AP000006; NID:G3236133; PDB:BAA30759.1; PID:G325

A:Experimental source: strain OT3

A>Note: this accession replaces an interim accession for a sequence replaced by GenBank

C:Genetics:

A:Gene: PH1547

C:Superfamily: molybdenum cofactor biosynthesis protein, MoeA type

Query Match 1.3%; Score 7; DB 2; Length 396;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 ILDDIP 83
|||
Db 331 ILDDIP 337

RESULT 50

URXLA1

peptidylglycine monooxygenase (EC 1.14.17.3) I precursor - African clawed frog

N:Alternate names: C-terminal alpha-amidating enzyme AE-I; peptidyl alpha-amidating enzy

C:Species: *Xenopus laevis* (African clawed frog)

C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004

C:Accession: A29726; S54374

R:Matsumoto, K.; Ohnuki, K.; Wada, Y.; Fuchimura, K.; Tanaka, S.; Matsuo, H.

Biochem. Biophys. Res. Commun. 148, 546-552, 1987

A:Title: Cloning and sequence of cDNA encoding a peptidyl C-terminal alpha-amidating enzy

A:Reference number: A29726; MUID:88076923; PMID:3689360

A:Accession: A29726

A:Molecule type: mRNA

A:Residues: 1-400 <MTZ>

A:Cross-references: UNIPROT:P08478; GB:M33461

A:Experimental source: skin

A:Accession: S54374

A:Molecule type: Protein

A:Residues: 38-51;82-96;146-153;174-178;189-193;237-250;256-288;359-381 <MTW>

A:Experimental source: skin

C:Function: catalyzes oxidation of peptidylglycine to the corresponding peptidyl(2-hy

A:Description: catalyzes oxidation of peptidylglycine to the corresponding peptidyl(2-hy

A:Note: C-terminal alpha-amide structure is essential for the biological activity of many

C:Superfamily: peptidylglycine monooxygenase I; peptidylglycine monooxygenase I homolog

C:Keywords: copper; monooxygenase; oxidoreductase

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-37/Domain: propeptide #status predicted <PRO>

F:38-381/Product: peptidylglycine monooxygenase I #status experimental <MAT>

F:131-342/Domain: peptidylglycine monooxygenase I homolog <FGM>

F:382-400/Domain: carboxyl-terminal propeptide #status predicted <CTP>

Query Match 1.3%; Score 7; DB 1; Length 400;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 NIPSTSD 92
|||
Db 111 NIPSTSD 117

RESULT 51

F75275

chromate transport protein - *Deinococcus radiodurans* (strain R1)

C:Species: *Deinococcus radiodurans*

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: F75275

R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; S.

M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; Mah

Science 285, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.

A:Reference number: A75250; MUID:20036896; PMID:10567266

A:Accession: F75275

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-400 <WHI>

A:Cross-references: UNIPROT:Q9R8S2; GB:AE002072; GB:AE000513; NID:G6460231; PDB:AA11955

A:Experimental source: strain R1

C:Genetics:

A:Gene: DR2413

A:Map position: 1

Query Match 1.3%; Score 7; DB 2; Length 400;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 331 GLVWLP 337
|||
Db 216 GLVWLP 222

RESULT 52

C83464
hypothetical protein PA1441 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: C83464
R:Stover, C.K.; Pham, X.Q.; Ervin, A.L.; Mitsuuchi, S.D.; Warren, P.; Hickey, M.J.; B
adman, S.; Yuen, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lartig, K.; Lam,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: C83464
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-427 <STO>
A:Cross-references: UNIPROT:Q91306; GB:AE004574; GB:AE004091; NID:g9947391; PIDN:AA0483
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA1441

Query Match 1.3%; Score 7; DB 2; Length 427;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 GDEPITLA 64
DB 399 GDEPITLA 405

RESULT 53
D70468
conserved hypothetical protein eq_1964 - Aquifex aeolicus
C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C:Accession: D70468
R:Beckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O
V.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320
A:Accession: D70468
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-429 <AO>
A:Cross-references: UNIPROT:O67776; GB:AE000765; NID:g2984199; PIDN:AA07743.1; PID:g298
A:Experimental source: strain VFS
C:Genetics:
A:Gene: eq_1964
C:Superfamily: Escherichia coli probable zinc proteinase yael

Query Match 1.3%; Score 7; DB 2; Length 429;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 126 GQAAQSG 132
DB 346 GQAAQSG 352

RESULT 54
H84826
hypothetical protein At2g40230 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: H84826
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bent, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanden, S.E.; Umayam, L.; Tallon, L.
euser, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: H84826
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-433 <STO>
A:Cross-references: UNIPROT:Q9XEF2; GB:AE002093; NID:g6598942; PIDN:AA18737.1; GSPDB:GN
A:Genetics:
A:Gene: At2g40230
A:Map position: 2

Query Match 1.3%; Score 7; DB 2; Length 433;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 351 SVLSLSA 357
DB 22 SVLSLSA 28

RESULT 55
H87329
conserved hypothetical protein CC0651 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: H87329
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.U.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete genome sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: H87329
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-436 <STO>
A:Cross-references: UNIPROT:Q9AFA0; GB:AE005673; NID:g13421866; PIDN:AAK2636.1; GSPDB:GN
A:Genetics:
A:Gene: CC0651

Query Match 1.3%; Score 7; DB 2; Length 436;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 377 LRDFRDN 383
DB 253 LRDFRDN 259

RESULT 56
G96945
similar to ABC transporter (permease) CAC0374 [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C:Accession: G96945
R:Rolling, J.; Breton, G.; Omelchenko, M.V.; Makarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: G96945
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-438 <KOR>
A:Cross-references: UNIPROT:Q97W26; GB:AE001437; PIDN:AAK78354.1; PID:g15023223; GSPDB:GN
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC0374

Query Match 1.3%; Score 7; DB 2; Length 438;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 271 IRSVKRL 277
DB 344 IRSVKRL 350

RESULT 57

S67437

Damage and replication checkpoint control protein - fission yeast (Schizosaccharomyces fission)

N:Alternate names: WD repeat containing protein Ctr3

C:Species: Schizosaccharomyces pombe

C>Date: 20-Jul-1996 #sequence revision 13-Mar-1997 #text_change 16-Aug-2004

C/Accession: T37658; T43281; S67437

R/Comment: R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.

submitted to the EMBL Data Library, February 1996

A:Reference number: 221732

A:Accession: T37658

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-446 <CO2>

A/Cross-references: UNIPROT:Q10272; EMBL:Z69729; NID:g1204167; PIDN:CAA93596.1; PID:e223

A:Experimental source: strain 972h; cosmid C1367

R/Saka, Y.; Esashi, F.; Matsusaka, T.; Mochida, S.; Yanagida, M.

Genes Dev. 11, 3387-3400, 1997

A>Title: Damage and replication checkpoint control in fission yeast is ensured by intera

A:Reference number: 222390; MUID:98070339; PMID:9407031

A:Accession: T43281

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A/Cross-references: EMBL:AB008572; PIDN:BA23358.1

C/Genetics:

A:Gene: SPAC1367.08c; ctr3+

A:Map position: 1

A:Insertion: 66/3; 403/3

C/Function:

A:Description: may be involved in G1/S progression

A>Note: essential for viability

C:Superfamily: WD repeat homology

F:292-325/Domain: WD repeat homology <MDL>

Query Match	1.3%;	Score 7;	DB 2;	Length 446;
Best Local Similarity	100.0%;	Pred. No. 1.2e+02;		
Matches	7;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;

Oy	362	LFTASND	368
Db	133	LFTASND	139

RESULT 58

GMEBT

Indole-3-glycerol-phosphate synthase (EC 4.1.1.48) / phosphoribosylanthranilate isomerase

N:Contains: indole-3-glycerol-phosphate synthase (EC 4.1.1.48); phosphoribosylanthranilate

C/Species: Salmonella typhimurium

C>Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 09-Jul-2004

C/Accession: A01132

R/Horowitz, H.; Van Arsdell, J.; Platt, T.

J. Mol. Biol. 169, 775-797, 1983

A>Title: Nucleotide sequence of the trpD and trpC genes of Salmonella typhimurium.

A:Reference number: A92907; MUID:84036180; PMID:6355484

A:Accession: A01132

A:Molecule type: DNA

A/Residues: 1-452 <HOR>

A/Cross-references: UNIPROT:P00910; GB:M30286; NID:g154394; PIDN:AAA27237.1; PID:g154397

C/Genetics:

A:Gene: trpC-trpF

A:Map position: 34 min

C/Function: <PPAI>

A:Description: phosphoribosylanthranilate isomerase catalyzes conversion of N-5'-phospho

A:Pathway: tryptophan biosynthesis

A>Note: third step; catalyzed by the trpF homology domain

C/Function: <IGPS>

A:Description: indole-3-glycerol phosphate synthase catalyzes the ring closure to indol-

A:Pathway: tryptophan biosynthesis

A>Note: fourth step; catalyzed by the trpC homology domain

C:Superfamily: trpC-trpF bifunctional enzyme; trpC homology; trpF homology

C:Keywords: carbon-carbon lyase; carboxy-lyase; intramolecular oxidoreductase; isomerase

F:4-252/Domain: trpC homology <TRC>
F:258-449/Domain: trpF homology <TRF>

Query Match	1.3%;	Score 7;	DB 1;	Length 452;
Best Local Similarity	100.0%;	Pred. No. 1.2e+02;		
Matches	7;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;

Oy	352	VLSLSAV	358
Db	325	VLSLSAV	331

RESULT 59

AD0653

Indole-3-glycerol phosphate synthase [imported] - Salmonella enterica subsp. enterica ser

C/Species: Salmonella enterica subsp. enterica serovar Typh

A>Note: this species has also been called Salmonella typhi

C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C/Accession: AD0653

R/Parthill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher,

th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,

S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A>Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

A:Reference number: AB0502; MUID:21534947; PMID:11677608

A:Accession: AD0653

A:Status: preliminary

A:Molecule type: DNA

A/Residues: 1-452 <PAR>

A/Cross-references: GB:AL513382; PIDN:CAD08407.1; PID:g16502450; GSPDB:GN00176

C/Genetics:

A:Gene: STY1326

C:Superfamily: trpC-trpF bifunctional enzyme; trpC homology; trpF homology

Query Match	1.3%;	Score 7;	DB 2;	Length 452;
Best Local Similarity	100.0%;	Pred. No. 1.2e+02;		
Matches	7;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;

Oy	352	VLSLSAV	358
Db	325	VLSLSAV	331

RESULT 60

S50725

Hypothetical protein YNL206c - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein NI346

C/Species: Saccharomyces cerevisiae

C>Date: 23-Aug-1995 #sequence_revision 19-Jan-1996 #text_change 09-Jul-2004

C/Accession: S50725; S63163; S49863

R/Domaux, U.L.; Coster, F.; Purnelle, B.; Goffeau, A.

Yeast 10, 1639-1645, 1994

A>Title: A 21.7 kb DNA segment on the left arm of yeast chromosome XIV carries WHI3, GCR2

A:Reference number: S50712; MUID:95242839; PMID:7725799

A:Accession: S50725

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A/Residues: 1-455 <DON>

A/Cross-references: UNIPROT:P40161; EMBL:X78898; NID:g600045; PIDN:CA55502.1; PID:g60005

R/Coster, F.; Domaux, U.L.; Goffeau, A.; Purnelle, B.; Van Dyck, L.

submitted to the Protein Sequence Database, April 1996

A:Reference number: S63151

A:Accession: S63163

A:Molecule type: DNA

A/Residues: 1-455 <COS>

A/Cross-references: EMBL:Z71482; NID:g1302206; PID:e239612; PID:g1302207; MIPS:YNL206C

A:Experimental source: strain S288C

C/Genetics:

A:Gene: SGD:RTT106

A/Cross-references: SGD:S0005150

A:Map position: 14L

Query Match 1.3%; Score 7; DB 2; Length 455;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Gaps 0;

OY 144 QNFEAES 150
 |||||
 DB 358 QNFEAES 364

RESULT 61

hypothetical protein CPJ1070 [imported] - Chlamydia pneumoniae (strain J138)

C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C:Accession: C86624
 R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ise
 Nucleic Acids Res. 28: 2311-2314, 2000
 A:Title: Comparison of whole genome sequences of Chlamydia pneumoniae J138.
 A:Reference number: A86491; MUID:20330349; PMID:10871362
 A:Accession: C86624
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-456 <STO>
 A:Cross-references: UNIPROT:Q92619; GB:BA000008; NID:98979443; PIDN:BA99277.1; GSFD:GN
 A:Experimental source: strain J138
 C:Genetics:
 A:Gene: CPJ1070

Query Match 1.3%; Score 7; DB 2; Length 455;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Gaps 0;

OY 301 LQKLSRL 307
 |||||
 DB 288 LQKLSRL 294

RESULT 62

hypothetical protein CP0780 [imported] - Chlamydia pneumoniae (strains CWL029 and AR

C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C:Accession: H72000; A81538
 R:Kalan, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
 Nature Genet. 21: 385-389, 1999
 A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
 A:Reference number: A72000; MUID:99206606; PMID:10192388
 A:Accession: H72000
 A:Molecule type: DNA
 A:Residues: 1-456 <ARN>
 A:Cross-references: UNIPROT:Q92619; GB:AE001687; GB:AE001363; NID:94377398; PIDN:AA01920
 A:Experimental source: strain CWL029
 R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hickey,
 C.; Dodson, R.; Gwin, M.; Nelson, W.; Deboy, R.; McClarty, G.; Salberg,
 Nucleic Acids Res. 28: 1397-1406, 2000
 A:Title: Genome sequences of Chlamydia trachomatis Mdn and Chlamydia pneumoniae AR39.
 A:Reference number: A81500; MUID:20150255; PMID:10684935
 A:Accession: A81538

A:Molecule type: DNA
 A:Residues: 1-456 <REA>
 A:Cross-references: GB:AE002236; GB:AE002161; NID:97189693; PIDN:AAF38579.1; PID:G718969
 A:Experimental source: strain AR39, HL cells
 C:Genetics:
 A:Gene: CPJ1070; CP0780

Query Match 1.3%; Score 7; DB 2; Length 456;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Gaps 0;

OY 301 LQKLSRL 307
 |||||
 DB 288 LQKLSRL 294

RESULT 63

hypothetical protein At2g31130 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C:Accession: H84716
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Varkken, S.E.; Unayam, L.; Tallon, L.;
 Neus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402: 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: H84716
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-457 <STO>
 A:Cross-references: UNIPROT:O82271; GB:AE002093; NID:93746063; PIDN:AA063838.1; GSFD:GN
 A:Genetics:
 A:Gene: At2g31130
 A:Map position: 2

Query Match 1.3%; Score 7; DB 2; Length 457;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Gaps 0;

OY 103 QPSLATS 109
 |||||
 DB 290 QPSLATS 296

RESULT 64

trab protein homolog - Spingomonas aromaticivorans plasmid pNL1

C:Species: Spingomonas aromaticivorans
 C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
 C:Accession: T31237
 R:Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sensen, C.W.; Ge
 submitted to the EMBL Data Library, July 1998
 A:Description: Complete sequence of a 184 kb catabolic plasmid from Spingomonas aromatic
 A:Reference number: Z20992
 A:Accession: T31237
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-458 <ROM>
 A:Cross-references: UNIPROT:O85945; EMBL:AF079317; NID:93378261; PID:93378378; PIDN:AA00:
 C:Genetics:
 A:Genome: plasmid pNL1
 A:Note: trab

Query Match 1.3%; Score 7; DB 2; Length 458;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Gaps 0;

OY 125 QGQAQNS 131
 |||||
 DB 130 QGQAQNS 136

RESULT 65

probable outer membrane efflux lipoprotein lbeB [imported] - Yersinia pestis (strain CO92

C:Species: Yersinia pestis
 C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
 C:Accession: AB0423
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
 de Lencastre, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
 H. M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett, T.
 Nature 413: 523-527, 2001
 A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A:Reference number: AB0001; MUID:21470413; PMID:11586360
 A:Accession: AB0423
 A:Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-468 <XLR>
 A:Cross-references: UNIPROT:Q82BD5; GB:AL590842; P1DN:CA092710.1; PID:g15981405; GSPDB:C
 C:Species: Mus musculus (house mouse)
 C:Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
 C:Accession: S43294
 R:Storm, E.E.; Huynh, T.V.; Copeland, N.G.; Jenkins, N.A.; Kingsley, D.M.; Lee, S.J.
 A:Title: Limb alterations in brachypodism mice due to mutations in a new member of the T
 A:Reference number: S43294; MUID:94195427; PMID:8145850
 A:Accession: S43294
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-495 <STO>
 A:Cross-references: UNIPROT:P43027; GB:U08337; NID:g488461; P1DN:AAA18778.1; PID:g488462
 C:Superfamily: Inhibin

Query Match 1.3%; Score 7; DB 2; Length 468;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 184 ETLVOSA 190
 |||||
 Db 221 ETLVOSA 227

RESULT 66
 S43294
 bone morphogenetic protein-related protein (GDF5) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
 C:Accession: S43294
 R:Storm, E.E.; Huynh, T.V.; Copeland, N.G.; Jenkins, N.A.; Kingsley, D.M.; Lee, S.J.
 A:Title: Limb alterations in brachypodism mice due to mutations in a new member of the T
 A:Reference number: S43294; MUID:94195427; PMID:8145850
 A:Accession: S43294
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-495 <STO>
 A:Cross-references: UNIPROT:P43027; GB:U08337; NID:g488461; P1DN:AAA18778.1; PID:g488462
 C:Superfamily: Inhibin

Query Match 1.3%; Score 7; DB 2; Length 495;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 346 LLDVRSV 352
 |||||
 Db 271 LLDVRSV 277

RESULT 67
 C85789
 hypothetical protein 'yeaJ [imported] - Escherichia coli (strain O157:H7, substrain EDL933
 C:Species: Escherichia coli
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
 C:Accession: C85789
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
 Nature 409, 528-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: C85789
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-496 <STO>
 A:Cross-references: UNIPROT:Q8XDT6; GB:AE005174; NID:G12515823; P1DN:AA656775.1; GSPDB:C
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: 'yeaJ
 C:Superfamily: hypothetical protein b1786

Query Match 1.3%; Score 7; DB 2; Length 496;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 369 PLWRF 375
 |||||
 Db 255 PLWRF 261

RESULT 68

JC2347
 growth/differentiation factor 5 - human
 C:Species: Homo sapiens (man)
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
 C:Accession: JC2347
 R:Hoeltgen, G.; Neidhardt, H.; Jacobowsky, B.; Pohl, J.
 Biochem. Biophys. Res. Commun. 204, 646-652, 1994
 A:Title: Cloning and expression of recombinant human growth/differentiation factor 5.
 A:Reference number: JC2347; MUID:95071375; PMID:7980526
 A:Accession: JC2347
 A:Molecule type: DNA
 A:Residues: 1-501 <HOE>
 A:Cross-references: UNIPROT:P43026; GB:X80915; NID:9671524; P1DN:CAA56874.1; PID:9671525
 C:Genetics:
 A:Gene: GDB:BMP9
 A:Cross-references: GDB:433948
 A:Introns: 211/1
 C:Superfamily: Inhibin
 C:Keywords: glycoprotein
 F:189/Binding site: carbohydrate (asn) (covalent) #status predicted
 F:381/382/Cleavage site: Arg-Ala (unidentified proteinase) #status predicted

Query Match 1.3%; Score 7; DB 2; Length 501;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 346 LLDVRSV 352
 |||||
 Db 277 LLDVRSV 283

RESULT 69
 A55452
 cartilage-derived morphogenetic protein 1 precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 09-Jul-2004
 C:Accession: A55452
 R:Chang, S.C.; Hoang, B.; Thomas, J.T.; Vukicevic, S.; Luyten, F.P.; Ryba, N.J.P.; Kozak,
 J. Biol. Chem. 269, 28227-28234, 1994
 A:Title: Cartilage-derived morphogenetic proteins. New members of the transforming growth
 A:Reference number: A55452; MUID:95050604; PMID:7961761
 A:Accession: A55452
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-501 <CHA>
 A:Cross-references: UNIPROT:P43026; GB:U13660; NID:9600731; PID:9600732
 C:Genetics:
 A:Gene: GDB:CDMP1
 A:Cross-references: GDB:438940
 C:Superfamily: Inhibin

Query Match 1.3%; Score 7; DB 2; Length 501;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 346 LLDVRSV 352
 |||||
 Db 277 LLDVRSV 283

RESULT 70
 T20121
 hypothetical protein F1A3.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T20121; T20742
 R:McMurray, A.
 submitted to the EMBL Data Library, April 1996
 A:Reference number: Z19225
 A:Accession: T20121
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-529 <WIL>

A;Cross-references: UNIPROT:Q18746; EMBL:Z70750; PIDN:CAA94749.1; GSPDB:GN00023; CESP:FL1A3
 A;Experimental source: clone C50F4
 R;McMurray, A.
 Submitted to the EMBL Data Library, April 1996
 A;Reference number: Z19318
 A;Accession: T20742
 A;Status: preliminary; translated from GB/EMBL/DDBT
 A;Molecule type: DNA
 A;Residues: 1-529 <M12>
 A;Cross-references: EMBL:Z70751; PIDN:CAA94752.1; GSPDB:GN00023; CESP:FL1A3.2
 A;Experimental source: clone FL1A3
 C;Genetics:
 A;Gene: CESP:FL1A3.2
 A;Map position: 5
 A;Intons: 18/3; 64/3; 87/1; 188/1; 260/3; 429/3; 478/3
 Query Match
 Best Local Similarity 100.0%; Score 7; DB 2; Length 529;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 5 VRLIKRT 11
 Db 310 VRLIKRT 316
 RESULT 71
 S74703
 hypothetical protein slr1301 - *Synechocystis* sp. (strain PCC 6803)
 C;Species: *Synechocystis* sp.
 A;Variety: PCC 6803
 C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
 C;Accession: S74703
 R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
 O., K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
 DNA Res. 3, 109-136, 1996
 A;Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*
 sp.
 A;Reference number: S74322; MUID:97061201; PMID:8905231
 A;Accession: S74703
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-535 <KAN>
 A;Cross-references: UNIPROT:P72839; EMBL:D90901; GB:AB001339; NID:91651897; PIDN:BA1685
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C;Genetics:
 A;Start codon: GTG
 Query Match
 Best Local Similarity 100.0%; Score 7; DB 2; Length 535;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 301 LQKLSRL 307
 Db 82 LQKLSRL 88
 RESULT 72
 T49074
 hypothetical protein F4F15.60 - *Arabidopsis thaliana*
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
 C;Accession: T49074
 R;Alcazar, J.P.; Clabault, G.; Cotter, A.; Maché, R.; Mewes, H.W.; Rudd, S.; Lemcke, K.;
 submitted to the Protein Sequence Database, April 2000
 A;Reference number: Z25015
 A;Accession: T49074
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-540 <ALC>
 A;Cross-references: UNIPROT:Q9SV09; EMBL:AL049711; GSPDB:GN00061; ATSP:F4F15.60
 A;Experimental source: cultivar Columbia; BAC clone F4F15
 C;Genetics:
 A;Gene: ATSP:F4F15.60

A;Map position: 3
 A;Intons: 225/2; 280/2; 342/2; 365/1; 461/2; 521/2
 Query Match
 Best Local Similarity 100.0%; Score 7; DB 2; Length 540;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 495 LPRGCGP 501
 Db 528 LPRGCGP 534
 RESULT 73
 C86264
 protein F3F19.5 [imported] - *Arabidopsis thaliana*
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C;Accession: C86264
 R;Theologis, A.; Becker, J.R.; Palm, C.J.; Federpsiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 Jensen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A;Authors: Hunter, J.D.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.
 A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A;Reference number: A86141; MUID:21016719; PMID:11130712
 A;Accession: C86264
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-547 <STO>
 A;Cross-references: UNIPROT:Q9SAD8; GB:AB005172; NID:94850386; PIDN:AAD1056.1; GSPDB:GN0
 C;Genetics:
 A;Gene: F3F19.5
 A;Map position: 1
 Query Match
 Best Local Similarity 100.0%; Score 7; DB 2; Length 547;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 346 LIDVRSV 352
 Db 440 LIDVRSV 446
 RESULT 74
 B64939
 hypothetical protein b1786 - *Escherichia coli* (strain K-12)
 C;Species: *Escherichia coli*
 C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
 C;Accession: B64939
 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
 A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A;Title: The complete genome sequence of *Escherichia coli* K-12.
 A;Reference number: A64720; MUID:97426617; PMID:9278503
 A;Accession: B64939
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-556 <BLAT>
 A;Cross-references: GB:AB000273; GB:U00096; NID:91788078; PIDN:AACT4856.1; PID:91788086;
 A;Experimental source: strain K-12, substrain MG1655
 C;Superfamily: hypothetical protein b1786
 Query Match
 Best Local Similarity 100.0%; Score 7; DB 2; Length 556;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 369 PLIMRFL 375
 Db 315 PLIMRFL 321

RESULT 75

G90940
hypothetical protein ECs2495 [imported] - Escherichia coli (strain O157:H7, substrain R1
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: G90940
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
Sasawara, N.; Yasunaga, T.; Kuhtara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A:Reference number: A96629; MUID:21156231; PMID:11258796
A:Accession: G90940
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-556 <HAY>
A:Cross-references: UNIPROT:Q8XDT6; GB:BA000007; PIDN:BA835918.1; PID:913361962; GSEDB:G
A:Experimental source: strain O157:H7, substrain R1MD 0509952
C:Genetics:
A:Gene: ECs2495
C:Superfamily: hypothetical protein b1786

Query Match 1.3%; Score 7; DB 2; Length 556;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 369 PLWRF 375
DB 315 PLWRF 321

Search completed: November 16, 2004, 07:32:28
Job time : 48 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2004, 07:21:20 ; Search time 195 Seconds
(without alignments)
1540.234 Million cell updates/sec

Title: US-09-927-458-2

Perfect score: 522
Sequence: 1 MKLRVRLKRTWPLEVETE.....DRFPPRPSRGRTDGRLSFM 522

Scoring table: OLIGO
Gapop 60.0 , Gapept 60.0

Searched: 1825181 segs, 575374646 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database: UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	490	93.9	522	1	FBX7_HUMAN
2	490	93.9	522	1	CAG30377
3	31	5.9	361	2	O6Y017
4	31	5.9	361	2	AAP83452
5	26	5.0	523	2	O8K0A5
6	11	2.1	478	2	O6D859
7	10	1.9	1265	2	O86H88
8	8	1.5	185	2	O8M223
9	8	1.5	200	2	O6U7Y3
10	8	1.5	200	2	AA074304
11	8	1.5	300	2	O6BKS6
12	8	1.5	331	2	O768P2
13	8	1.5	331	2	BAD17904
14	8	1.5	353	2	O62197
15	8	1.5	355	2	O6NA16
16	8	1.5	355	2	CAE26813
17	8	1.5	402	1	VE2_HPV65
18	8	1.5	404	2	O702V2
19	8	1.5	404	2	CAF25097
20	8	1.5	628	2	O9J133
21	8	1.5	686	2	O98F09
22	8	1.5	730	2	O9SKK7
23	8	1.5	758	2	O704C4
24	8	1.5	1047	2	O74BPI
25	8	1.5	1047	2	AAR35321
26	7	1.3	67	2	O8TJ06
27	7	1.3	67	2	O8SNT0
28	7	1.3	80	2	O7R6Q1
29	7	1.3	80	2	O76H60
30	7	1.3	80	2	BAD15208
31	7	1.3	82	2	O7P7A6

32	7	1.3	84	2	P74781	P74781 synchocyst
33	7	1.3	89	2	O9G218	O9G218 eretmocerus
34	7	1.3	89	2	O9G966	O9G966 eretmocerus
35	7	1.3	91	2	O6GV22	O6GV22 bos taurus
36	7	1.3	91	2	O9ZV53	O9ZV53 arabidopsis
37	7	1.3	91	2	O89TW2	O89TW2 bradyrhizob
38	7	1.3	92	2	O6YMB6	O6YMB6 oryza sativ
39	7	1.3	92	2	BAD17403	BAD17403 oryza sat
40	7	1.3	96	2	BAD17570	BAD17570 oryza sat
41	7	1.3	96	2	O9Y0B7	O9Y0B7 pyrococcus
42	7	1.3	105	2	O81E48	O81E48 bacillus ce
43	7	1.3	110	2	O54878	O54878 streptococc
44	7	1.3	111	2	O8MT79	O8MT79 drosophila
45	7	1.3	112	2	O9ANA6	O9ANA6 bradyrhizob
46	7	1.3	118	2	O8HA88	O8HA88 bacterioph
47	7	1.3	120	2	O8CLJ3	O8CLJ3 yersinia pe
48	7	1.3	123	2	O8CIU9	O8CIU9 mus musculu
49	7	1.3	125	2	O81RB0	O81RB0 bacillus an
50	7	1.3	125	2	AAT31258	AAT31258 bacillus
51	7	1.3	131	1	SSB2_STR3	SSB2_STR3
52	7	1.3	131	1	SSB2_STR5	SSB2_STR5
53	7	1.3	140	2	O8ZE27	O8ZE27 yersinia pe
54	7	1.3	140	2	AA662066	AA662066 yersinia
55	7	1.3	141	2	O973V4	O973V4 sulfolobus
56	7	1.3	141	2	O8C938	O8C938 mus musculu
57	7	1.3	144	2	O6XIE4	O6XIE4 drosophila
58	7	1.3	144	2	O8ABP0	O8ABP0 bacteroides
59	7	1.3	144	2	AAR09909	AAR09909 drosophil
60	7	1.3	148	2	O8GDK1	O8GDK1 photorhabdu
61	7	1.3	149	2	O94173	O94173 oryza sativ
62	7	1.3	150	1	Y487_MYCPN	Y487_MYCPN
63	7	1.3	151	2	O33VE4	O33VE4 oryza sativ
64	7	1.3	152	2	O7X9T7	O7X9T7 geum rivale
65	7	1.3	160	1	PHAA_ANAC	PHAA_ANAC
66	7	1.3	160	1	PHAA_FREDI	PHAA_FREDI
67	7	1.3	160	1	PHAA_PORFE	PHAA_PORFE
68	7	1.3	160	2	O8DU53	O8DU53 streptococc
69	7	1.3	163	2	O96MM0	O96MM0 homo sapien
70	7	1.3	166	2	O7OIG5	O7OIG5 anopheles g
71	7	1.3	166	2	O8G4L5	O8G4L5 bifidobacte
72	7	1.3	167	2	O9TH82	O9TH82 clostridium
73	7	1.3	170	2	O7V177	O7V177 prochloroco
74	7	1.3	172	2	O8T018	O8T018 drosophila
75	7	1.3	182	2	O7XJ34	O7XJ34 brassica ra
76	7	1.3	182	2	O8TVY3	O8TVY3 pseudomonas
77	7	1.3	182	2	O7TNH9	O7TNH9 caenoraba
78	7	1.3	184	2	O71H49	O71H49 andrena acc
79	7	1.3	184	2	O92BK4	O92BK4 listeria in
80	7	1.3	184	2	AA007600	AA007600 andrena a
81	7	1.3	185	2	O8MZV7	O8MZV7 spodoptera
82	7	1.3	185	2	O8MZW3	O8MZW3 spodoptera
83	7	1.3	187	2	O6KAO0	O6KAO0 oryza sativ
84	7	1.3	187	2	O8ET53	O8ET53 caenorabaci
85	7	1.3	187	2	O9EX11	O9EX11 caenorabaci
86	7	1.3	188	2	O71GN9	O71GN9 andrena vic
87	7	1.3	188	2	O71GPI	O71GPI andrena nly
88	7	1.3	188	2	O71GPI	O71GPI andrena dol
89	7	1.3	188	2	O71GZ1	O71GZ1 andrena lem
90	7	1.3	188	2	O71GZ2	O71GZ2 andrena lev
91	7	1.3	188	2	O71H03	O71H03 andrena hum
92	7	1.3	188	2	O71H51	O71H51 andrena acc
93	7	1.3	188	2	O6HPR4	O6HPR4 bacillus th
94	7	1.3	188	2	O73F15	O73F15 bacillus ce
95	7	1.3	188	2	O81I29	O81I29 bacillus ce
96	7	1.3	188	2	O81VM9	O81VM9 bacillus an
97	7	1.3	188	2	AA539128	AA539128 bacillus
98	7	1.3	188	2	AA007598	AA007598 andrena a
99	7	1.3	188	2	AA007646	AA007646 andrena h
100	7	1.3	188	2	AA007656	AA007656 andrena l

ALIGNMENTS

```

RESULT 1
FBX7_HUMAN STANDARD; PRT; 522 AA.
AC O95YI1; O95H6; O95P21; O9UKT2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE F-box only protein 7.
GN Name=FBX07; Synonyms=FBX7;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CX NCBT_TaxID=9606;
RN [1]
RP SEQUENCE OF 41-522 FROM N.A.
RX MEDLINE=20003060; PubMed=10531035;
RA Cenciarelli C., Chatur D.S., Guardavaccaro D., Parks W., Vidal M.,
RA Pagano M.;
RL Curr. Biol. 9:1177-1179(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20399565; PubMed=10945468; DOI=10.1006/geno.2000.6211;
RA Ilyin G.P., Rialland M., Pigeon C., Guenou-Guillouzo C.;
RT "cDNA cloning and expression analysis of new members of the mammalian
RT F-box protein family";
RL Genomics 67:40-47(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20057165; PubMed=10591208; DOI=10.1038/990031;
RA Dunham I., Hunt A.R., Collins J.E., Bruskiewicz R., Beare D.M.,
RA Clump M., Smink L.J., Atscough R., Almeida J.P., Abbade A.K.,
RA Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
RA Burdill W.D., Burton V., Carder C., Carter N.P., Chen Y., Clark G.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson B.,
RA Evans K.D., Dockree C., Dodsworth S.J., Dublin R.M., Ellington A.G.,
RA Hammi P.L., Fey J.M., Fleming K., French L., Garner A.A.,
RA Gilbert J.G.R., Goward M.E., Graham D.V., Griffiths M.N.D., Hall C.,
RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA Laird G.K., Langford C.F., Leverisha M.A., Lloyd C., Lloyd D.M.,
RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA Mcclay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
RA Phillips S.H., Plumb R.W., Ramsey H., Ramsey Y., Rogers L., Ross M.T.,
RA Scott C.E., Seha H.K., Skuce C.D., Smalley S., Smith M.L.,
RA Soederlund C., Spragon L., Stewart C.A., Sulston J.E., Swann R.M.,
RA Vaadin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilmington L.,
RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA Mitoshima S., Kawasaki K., Sasaki T., Asakawa S., Kodoh J.,
RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.T.,
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,
RA Zhan Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
RA Zhan M., Zhang G., Chissos S., Murray J., Miller N., Minx P.,
RA Fulton R., Johnson D., Bemis G., Bentley D., Brashaw H., Bourne S.,
RA Cordes M., Da Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA Hinds K., Kemp K., Latreille P., Layman D., Olesky P., Rottling T.,
RA Schuet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J.,
RA Kofl I., Bedell J.A., Hillier L.W., Markis E., Waterston R.,
RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Salter S.,
RA Budarf M.L., Mcdermott H.E., Johnson A., Wong A.C.C., Morrow B.E.,
RA Edmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,
RA Peyrard M., Kedra D., Serousi E., Franssen I., Tapia I., Bruder C.E.,
RA O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,
RA Khan A.S., Lane L., Tiliun Y., Wright H.;
RT "The DNA sequence of human chromosome 22.";
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RL Nature 402:489-495(1999).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marzina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stadleron M., Soares M.B., Bonaldo M.F., Casavant T.J., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshlyuk S., Carninci P., Prange C.,
RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mulhaby S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy U., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzyzinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Matra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Probably recognizes and binds to some phosphorylated
CC proteins and promotes their ubiquitination and degradation.
CC -!- SUBUNIT: Part of a SCF (SKP1-cullin-F-box) protein ligase complex
CC (By similarity).
CC -!- SIMILARITY: Contains 1 F-box domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL, AF129537; AAF04471.1; -
DR EMBL, AF233225; AAF67155.1; -
DR EMBL, AL050254; CAB43356.1; -
DR EMBL, Z71183; CAB63143.1; -
DR EMBL, BC008361; AAH08361.1; -
DR Genev; HGNC:13586; FBX07.
DR GO; GO:0000151; C:ubiquitin ligase complex; TAS.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; TAS.
DR GO; GO:0006511; P:ubiquitin-dependent protein catabolism; TAS.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR008945; SKP1_Skp2.
DR Pfam; PF00646; F-box; 1.
DR PROSITE; PS50181; FBX07; 1.
DR Ubl conjugation pathway.
RN DOMAIN 329 375
FT CONFLICT 41 41 F-box.
FT CONFLICT 79 79 Q -> H (in Ref. 1).
FT CONFLICT 84 84 M -> P (in Ref. 1).
FT CONFLICT 115 115 M -> I (in Ref. 1 and 4).
FT CONFLICT 169 169 M -> L (in Ref. 1).
FT CONFLICT 224 224 P -> H (in Ref. 1).
FT CONFLICT 241 241 P -> N (in Ref. 1).
FT CONFLICT 328 328 M -> L (in Ref. 1).
FT CONFLICT 413 413 M -> L (in Ref. 1).
FT CONFLICT 475 475 F -> L (in Ref. 1).
SQ SEQUENCE 522 AA; 58502 MW; CAE5E70A074287A CRC64;
Query Match 93.9%; Score 490; DB 1; Length 522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 490; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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33 SLCTWGSYSSNTRFTITNYKOPITGDEETASGIYSGDILCLDIDIPAPNPISSTD 92

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Db      33 SLCTGWGSSNTRFTITLNYKDPDLPDDEETLASVYGVSGDLICLLQDDIPAPNIPSSTD 92
Qy      93 SEHSIQQNNEQBPPLATSSNOTSMQDEQPSPOGQAAGSGVWMDSDMGPSONFEASTQ 152
Db      93 SEHSIQQNNEQBPPLATSSNOTSMQDEQPSPOGQAAGSGVWMDSDMGPSONFEASTQ 152
Qy      153 DNAAHAGTGTFYSEBMLCSSEVGEQVPSHLETLVQSADCSNDALIVLHILMLESGY 212
Db      153 DNAAHAGTGTFYSEBMLCSSEVGEQVPSHLETLVQSADCSNDALIVLHILMLESGY 212
Qy      213 IPGTEAKALSMPEKMLSGVYKLQYMHPLCEGSSATLTCVPLGNLIVNATLKINNEIR 272
Db      213 IPGTEAKALSMPEKMLSGVYKLQYMHPLCEGSSATLTCVPLGNLIVNATLKINNEIR 272
Qy      273 SVKRLQLLPESFICKEKLGENVANITYKDLQKLSRLFKDQVLYPLAFTRCALNLPVFGI 332
Db      273 SVKRLQLLPESFICKEKLGENVANITYKDLQKLSRLFKDQVLYPLAFTRCALNLPVFGI 332
Qy      333 VVLPLELKRIFFRLDVRSVLSAVCRDLFTASNDPLMRFLYLDFPDNTYAVQDIDM 392
Db      333 VVLPLELKRIFFRLDVRSVLSAVCRDLFTASNDPLMRFLYLDFPDNTYAVQDIDM 392
Qy      393 KELYRKRIHQKESPKGRFVWLPPSSTHTIPFYENPLHPRFPSSRLPGIIGGEYDQRP 452
Db      393 KELYRKRIHQKESPKGRFVWLPPSSTHTIPFYENPLHPRFPSSRLPGIIGGEYDQRP 452
Qy      453 TLPPYGDPISSLIQPGGETPSQFPPLRPDPVGPLPGPNPLPGRGGNDPFRFRSRG 512
Db      453 TLPPYGDPISSLIQPGGETPSQFPPLRPDPVGPLPGPNPLPGRGGNDPFRFRSRG 512
Qy      513 RPTDGRLSFM 522
Db      513 RPTDGRLSFM 522

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RESULT 2

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CAG30377
ID CAG30377 PRELIMINARY; PRT; 522 AA.
AC CAG30377;
DT 01-JUN-2004 (TREMBlrel. 27, Created)
DT 01-JUN-2004 (TREMBlrel. 27, Last sequence update)
DE 01-JUN-2004 (TREMBlrel. 27, Last annotation update)
DE FBX07 protein.
GN FBX07.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Collins J.E., Wright C.L., Edwards C.A., Davis M.P., Githam J.A.,
RA Cole C.G., Goward M.E., Aguado B., Malliya M., Mokrab Y., Huckle E.J.,
RA Beare D.M., Dunham I.;
RA Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR456491; CAG30377.1; -
SQ SEQUENCE 522 AA; 58502 MW; CAEE570A0747287A CRC64;

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Query Match 93.9%; Score 490; DB 2; Length 522;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 490; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      33 SLCTGWGSSNTRFTITLNYKDPDLPDDEETLASVYGVSGDLICLLQDDIPAPNIPSSTD 92
Db      33 SLCTGWGSSNTRFTITLNYKDPDLPDDEETLASVYGVSGDLICLLQDDIPAPNIPSSTD 92
Qy      93 SEHSIQQNNEQBPPLATSSNOTSMQDEQPSPOGQAAGSGVWMDSDMGPSONFEASTQ 152
Db      93 SEHSIQQNNEQBPPLATSSNOTSMQDEQPSPOGQAAGSGVWMDSDMGPSONFEASTQ 152
Qy      213 IPGTEAKALSMPEKMLSGVYKLQYMHPLCEGSSATLTCVPLGNLIVNATLKINNEIR 272
Db      213 IPGTEAKALSMPEKMLSGVYKLQYMHPLCEGSSATLTCVPLGNLIVNATLKINNEIR 272
Qy      273 SVKRLQLLPESFICKEKLGENVANITYKDLQKLSRLFKDQVLYPLAFTRCALNLPVFGI 332
Db      273 SVKRLQLLPESFICKEKLGENVANITYKDLQKLSRLFKDQVLYPLAFTRCALNLPVFGI 332
Qy      393 KELYRKRIHQKESPKGRFVWLPPSSTHTIPFYENPLHPRFPSSRLPGIIGGEYDQRP 452
Db      393 KELYRKRIHQKESPKGRFVWLPPSSTHTIPFYENPLHPRFPSSRLPGIIGGEYDQRP 452
Qy      453 TLPPYGDPISSLIQPGGETPSQFPPLRPDPVGPLPGPNPLPGRGGNDPFRFRSRG 512
Db      453 TLPPYGDPISSLIQPGGETPSQFPPLRPDPVGPLPGPNPLPGRGGNDPFRFRSRG 512
Qy      513 RPTDGRLSFM 522
Db      513 RPTDGRLSFM 522

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Qy      213 IPGTEAKALSMPEKMLSGVYKLQYMHPLCEGSSATLTCVPLGNLIVNATLKINNEIR 272
Db      213 IPGTEAKALSMPEKMLSGVYKLQYMHPLCEGSSATLTCVPLGNLIVNATLKINNEIR 272
Qy      273 SVKRLQLLPESFICKEKLGENVANITYKDLQKLSRLFKDQVLYPLAFTRCALNLPVFGI 332
Db      273 SVKRLQLLPESFICKEKLGENVANITYKDLQKLSRLFKDQVLYPLAFTRCALNLPVFGI 332
Qy      333 VVLPLELKRIFFRLDVRSVLSAVCRDLFTASNDPLMRFLYLDFPDNTYAVQDIDM 392
Db      333 VVLPLELKRIFFRLDVRSVLSAVCRDLFTASNDPLMRFLYLDFPDNTYAVQDIDM 392
Qy      393 KELYRKRIHQKESPKGRFVWLPPSSTHTIPFYENPLHPRFPSSRLPGIIGGEYDQRP 452
Db      393 KELYRKRIHQKESPKGRFVWLPPSSTHTIPFYENPLHPRFPSSRLPGIIGGEYDQRP 452
Qy      453 TLPPYGDPISSLIQPGGETPSQFPPLRPDPVGPLPGPNPLPGRGGNDPFRFRSRG 512
Db      453 TLPPYGDPISSLIQPGGETPSQFPPLRPDPVGPLPGPNPLPGRGGNDPFRFRSRG 512
Qy      513 RPTDGRLSFM 522
Db      513 RPTDGRLSFM 522

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RESULT 3

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Q6Y0L7
ID Q6Y0L7 PRELIMINARY; PRT; 361 AA.
AC Q6Y0L7;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE F-box only protein 7 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Emara M.G., Kim H.;
RA Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY194289; AAP83452.1; -
DR EMBL; AY194289; AAP83452.1; JOINED.
DR InterPro; IPR001810; F-box.
DR Pfam; PF00646; F-box; 1.
DR SMART; SM00256; FBOX; 1.
DR PROSITE; PS50181; FBOX; 1.
FT NON TER
SQ SEQUENCE 361 AA; 40110 MW; 51C54C0232833864 CRC64;

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Query Match 5.9%; Score 31; DB 2; Length 361;
 Best Local Similarity 100.0%; Pred. No. 2,6e-23;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      321 ROALNLPVPGVAVVLPLELKRIFFRLDVRVS 351
Db      169 ROALNLPVPGVAVVLPLELKRIFFRLDVRVS 199

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RESULT 4

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AAP83452
ID AAP83452 PRELIMINARY; PRT; 361 AA.
AC AAP83452;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DE 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE F-box only protein 7 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;

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RN [1]
RP SEQUENCE FROM N.A.
RA Emera M.G., Kim H.;
RT "Genomic region of P-box only protein 7 in chicken.";
RL Submitted (DSC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY194288; AAP83452.1; JOINED.
FT NON TER
SQ SEQUENCE 361 AA; 40110 MW; 51C54C0292833884 CRC64;

Query Match 5.9%; Score 31; DB 2; Length 361;
Best Local Similarity 100.0%; Pred. No. 2.6e-23;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 321 RQALNPDVFGVLVPLLEKLRIFRLDVS 351
    |||||
Db 169 RQALNPDVFGVLVPLLEKLRIFRLDVS 199

RESULT 5
08KOAS PRELIMINARY; PRT; 523 AA.
AC 08KOAS;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE F-box only protein 7.
OS Name=Fbox7;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=FVB/N; TISSUE=Liver;
RC MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stadelton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=FVB/N; TISSUE=Liver;
RC Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC032153; AAH32153.1; -.
DR MGD; MGI:1917004; Fbox7.
DR InterPro; IPR001810; F-box.
DR Pfam; PF00646; F-box; 1.
DR PROSITE; PS50181; FBOX; 1.
SQ SEQUENCE 523 AA; 57634 MW; AAFD250070C1FEB5 CRC64;

Query Match 5.0%; Score 26; DB 2; Length 523;
Best Local Similarity 100.0%; Pred. No. 7.2e-18;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 324 INLDPVFGVLVPLLEKLRIFRLDV 349

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Db 325 INLDPVFGVLVPLLEKLRIFRLDV 350
    |||||
RESULT 6
06DB59 PRELIMINARY; PRT; 478 AA.
AC 06DB59;
DT 01-OCT-2004 (TReMBLrel. 28, Created)
DT 01-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 01-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
CX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Embryo;
RC MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT Initiative";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=Embryo;
RC PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stadelton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RA STRAIN=Embryo;
RC Klein S., Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC077283; AAH77283.1; -.
DR Hypothetical protein.
SQ SEQUENCE 478 AA; 53251 MW; 8C12F01E32C1873F CRC64;

Query Match 2.1%; Score 11; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 338 ELKLRIFRLD 348
    |||||
Db 320 ELKLRIFRLD 330

RESULT 7
086HP8 PRELIMINARY; PRT; 1265 AA.
ID 086HP8;
AC 086HP8;
DT 01-JUN-2003 (TReMBLrel. 24, Created)

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DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostelidae; Dictyostelium.
 CX NCBI_TaxID=44689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AX4;
 RX MEDLINE=22092622; PubMed=12097910;
 RA Gloeckner G., Eichinger L., Szatranski K., Pachebat J., Dear P.,
 Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
 Rungsgal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.,
 RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.",
 RL Nature 418:79-85(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AX4;
 RA Baumgart C.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC116957; AA052522.1; -;
 DR InterPro: IPR002114; HPR_Ser_P_S.
 DR InterPro: IPR008940; Prenyl_Trans.
 DR PROSITE: PS00589; PTS_HPR_SER; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 1265 AA; 144025 MW; B925B8475526EB1C CRC64;

Query Match 1.5%; Score 10; DB 2; Length 1265;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 349 VRSVLSLSAV 358
 |||||
 Db 165 VRSVLSLSAV 174

RESULT 8
 Q8M2Z3 PRELIMINARY; PRT; 185 AA.
 ID Q8M2Z3;
 AC Q8M2Z3;
 DT 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE Acyl-CoA desaturase Hassksve (Fragment).
 OS Heliooverpa assulta (Oriental tobacco budworm).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Dictyssa; Noctuoidea;
 OC Noctuidae; Heliothinae; Helioverpa.
 CX NCBI_TaxID=52344;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22412134; PubMed=12524345;
 RA Knipfle D.C., Rosenfield C.L., Nielsen R., You K.M., Jeong S.E.;
 RT "Evolution of the integral membrane desaturase gene family in moths
 and flies.",
 RL Genetics 162:1737-1752(2002).
 DR EMBL: AF482907; AA028482.1; -;
 DR GO: GO:0005783; C:cytoplasmic reticulum; IEA;
 DR GO: GO:0016020; C:membrane; IEA;
 DR GO: GO:0005506; F:iron ion binding; IEA;
 DR GO: GO:0016491; F:oxidoreductase activity; IEA;
 DR GO: GO:000468; F:fatty acid desaturase activity; IEA;
 DR GO: GO:000633; F:fatty acid biosynthesis; IEA;
 DR InterPro: IPR001522; Desaturase.
 DR InterPro: IPR005804; Pa_desat.
 DR Pfam: PF00487; PA_desaturase; 1.
 DR PRINTS: PR00075; FACDSATRASE.
 FT NON_TER 1
 FT 185
 SQ SEQUENCE 185 AA; 21597 MW; 54B7BDA00FA36FF7 CRC64;

Query Match 1.5%; Score 8; DB 2; Length 185;
 Best Local Similarity 100.0%; Pred. No. 30;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 44 TRFTITLN 51
 |||||
 Db 136 TRFTITLN 143

RESULT 9
 ID Q6U7Y3 PRELIMINARY; PRT; 200 AA.
 AC Q6U7Y3;
 DT 05-JUL-2004 (TReMBLrel. 27, Created)
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
 DE Hypothetical protein hyp14.
 GN Name=hyp14;
 GN Crinipellis perniciosa.
 OS Crinipellis perniciosa.
 OG Mitochondrion.
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Agaricales; Tricholomataceae; Crinipellis.
 CX NCBI_TaxID=153609;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Fornighieri E.F., Sardinha-Pinto N., Cotomacci C., Araujo M.R.R.,
 RA Digampieri L.A., Garza-Zole M.F., Cursi D.E., Bertolin R.B.,
 RA Castro L.A.B., Gramacho K., Goes-Neto A., Goncalves M.S.,
 RA Barbosa L.V., Fernandez L.G., Cascardo J.C.M., Pereira G.A.G.,
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY376688; AA074304.1; -;
 DR GO: GO:0005739; C:mitochondrion; IEA.
 KW Hypothetical protein; Mitochondrion.
 SQ SEQUENCE 200 AA; 22038 MW; F7A99538A8A64D36 CRC64;

Query Match 1.5%; Score 8; DB 2; Length 200;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 349 VRSVLSLS 356
 |||||
 Db 87 VRSVLSLS 94

RESULT 10
 AA074304 PRELIMINARY; PRT; 200 AA.
 ID AA074304;
 AC AA074304;
 DT 03-MAR-2004 (TReMBLrel. 27, Created)
 DT 03-MAR-2004 (TReMBLrel. 27, Last sequence update)
 DT 03-MAR-2004 (TReMBLrel. 27, Last annotation update)
 DE Hypothetical protein hyp14.
 GN Name=hyp14;
 GN Crinipellis perniciosa.
 OS Crinipellis perniciosa.
 OG Mitochondrion.
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Agaricales; Tricholomataceae; Crinipellis.
 CX NCBI_TaxID=153609;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Fornighieri E.F., Sardinha-Pinto N., Cotomacci C., Araujo M.R.R.,
 RA Digampieri L.A., Garza-Zole M.F., Cursi D.E., Bertolin R.B.,
 RA Castro L.A.B., Gramacho K., Goes-Neto A., Goncalves M.S.,
 RA Barbosa L.V., Fernandez L.G., Cascardo J.C.M., Pereira G.A.G.,
 RT "The complete mitochondrial genome of Crinipellis perniciosa, the
 RT causal agent of witches' broom disease of cocoa.",
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY376688; AA074304.1; -;
 KW Hypothetical protein; Mitochondrion.
 SQ SEQUENCE 200 AA; 22038 MW; F7A99538A8A64D36 CRC64;

Query Match 1.5%; Score 8; DB 2; Length 200;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 349 VRSVLSTS 356
Db 87 VRSVLSTS 94

RESULT 11

Q6BK56 PRELIMINARY; PRT; 300 AA.
ID O6BK56
AC O6BK56
DT 01-OCT-2004 (TREMBlrel. 28, Created)
DT 01-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 01-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Similar to CA2573|CASU2 Candida albicans Casu2 translation
DE Initiation factor elf2.
GN ORFNames=DEHA0F262359;
OS Debaryomyces hansenii (Yeast) (Torulaspora hansenii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomyces.
OX NCBI_TaxID=4959;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS767;
RG GENOLIVURES;

RA Lafontaine I., de Montigny J., Marck C., Neveglisse C., Talla E.,
RA Goffard N., Fraigneul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boissiere A., Boyer J., Cattoir L., Confalonieri F., de Baruyar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantreya F., Hennequin C., Jaumaux N., Joyet P., Kachouri R.,
RA Kerret A., Kosul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikoleki M., Ozias S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Portier S., Richard G.F., Straub M.L., Suleau A.,
RA Swenne D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zentou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissendach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in Yeasts";
RL Nature 430:35-44 (2004).

RP SEQUENCE FROM N.A.
RC STRAIN=CBS767;
RG GENOSCOPE;

RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR382138; CAG89828.1; -
KW Initiation factor.
SQ SEQUENCE 300 AA; 33796 MW; 043AE9504267674B CRC64;

Query Match 1.5%; Score 8; DB 2; Length 300;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 182 SLETLVOS 189
Db 122 SLETLVOS 129

RESULT 12
Q76BF2 PRELIMINARY; PRT; 331 AA.
ID Q76BF2
AC Q76BF2
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Fructose-bisphosphate aldolase C (Fragment).
OS Leptostoeus osseus (Long-nosed gar).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Semionotiformes; Leptostetidae;
OC Leptostoeus.
OX NCBI_TaxID=34771;
RN [1]
RP SEQUENCE FROM N.A.
RC Kikugawa K., Katoh K., Kuraku S., Sakurai H., Ishida O., Iwabe N.,

RA Kikugawa K., Katoh K., Kuraku S., Sakurai H., Ishida O., Iwabe N.,

RA Miyata T.;
RT "Basal jawed vertebrate phylogeny inferred from multiple nuclear DNA-
RT coded genes.";
RL BMC Biol. 2:3-3 (2004).
DR EMBL; AB11390; BADI7904.1; -
DR InterPro; IPR000741; Aldolase_I.
DR Pfam; PF00274; Glycolytic_1.
DR Prodom; PD001128; Aldolase_I; 1.
DR PROSITE; PS00158; ALDOLASE_CLASS_I; 1.
FT NON_TER
SQ SEQUENCE 331 AA; 35835 MW; 26DB5C3FF4C3413A CRC64;

Query Match 1.5%; Score 8; DB 2; Length 331;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 184 ETLVOSAD 191
Db 49 ETLVOSAD 56

RESULT 13
BADI7904 PRELIMINARY; PRT; 331 AA.
ID BADI7904
AC BADI7904
DT 01-JUN-2004 (TREMBlrel. 27, Created)
DT 01-JUN-2004 (TREMBlrel. 27, Last sequence update)
DT 01-JUN-2004 (TREMBlrel. 27, Last annotation update)
DE Fructose-bisphosphate aldolase C (Fragment).
OS Leptostoeus osseus (Long-nosed gar).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Semionotiformes; Leptostetidae;
OC Leptostoeus.
OX NCBI_TaxID=34771;
RN [1]
RP SEQUENCE FROM N.A.
RC Kikugawa K., Katoh K., Kuraku S., Sakurai H., Ishida O., Iwabe N.,

RA Kikugawa K., Katoh K., Kuraku S., Sakurai H., Ishida O., Iwabe N.,
RA Miyata T.;
RT "Basal jawed vertebrate phylogeny inferred from multiple nuclear DNA-
RT coded genes.";
RL BMC Biol. 2:3-3 (2004).
DR EMBL; AB11390; BADI7904.1; -
FT NON_TER
SQ SEQUENCE 331 AA; 35835 MW; 26DB5C3FF4C3413A CRC64;

Query Match 1.5%; Score 8; DB 2; Length 331;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 184 ETLVOSAD 191
Db 49 ETLVOSAD 56

RESULT 14
O62197 PRELIMINARY; PRT; 353 AA.
ID O62197
AC O62197
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Hypothetical protein F32A11.3.
GN Name=F32A11.3;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for

RA none;
RT "Genome sequence of the nematode C.elegans: A platform for

RT Investigating biology.",
RL Science 282:2012-2018(1998).
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Smye R.;
RU Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z81521; CAB04225.1; -
DR PIR; T21616; T21616.
DR WormPep; F32A11.3; CE17739.
KM Hypothetical protein.
SQ SEQUENCE 353 AA; 38773 MW; 1435DF5F7C1F2416 CRC64;

Query Match 1.5%; Score 8; DB 2; Length 353;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 350 RSVSLSA 357
DB 53 RSVSLSA 60

RESULT 15
Q6NA16 PRELIMINARY; PRT; 355 AA.

DT 05-JUL-2004 (TREMblrel. 27, Created)
DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
DE Nitrogen-fixing NifU, C-terminal.
GN OrderedLocustNames=RPAL370;
OS Rhodopseudomonas palustris.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Rhodopseudomonas.
OX NCBI_TaxID=1076;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=CGA009 / ATCC BAA-98;
RX PubMed=14704707; DOI=10.1038/nbr1923;
RA Laimmer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,
RA Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,
RA Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Peres C.,
RA Harrison F.H., Gibson J., Harwood C.S.;
RT "Complete genome sequence of the metabolically versatile
RT photosynthetic bacterium Rhodopseudomonas palustris.";
RL Nat. Biotechnol. 22:55-61(2004).
DR EMBL; BX572597; CAE26813.1;
DR InterPro; IPR01075; NifU_C.
DR Pfam; PF01106; NifU; 1.
DR ProDom; PD002830; NifU_C; 1.
KM Complete proteome.
SQ SEQUENCE 355 AA; 39283 MW; 7E37E937A2E431F0 CRC64;

Query Match 1.5%; Score 8; DB 2; Length 353;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 LSAVCRDL 362
DB 98 LSAVCRDL 105

RESULT 16
CAE26813 PRELIMINARY; PRT; 355 AA.

AC CAE26813
DT 02-MAR-2004 (TREMblrel. 27, Created)
DT 02-MAR-2004 (TREMblrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMblrel. 27, Last annotation update)
DE Nitrogen-fixing NifU, C-terminal.
GN RPA1370.
OS Rhodopseudomonas palustris.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

OC Bradyrhizobiaceae; Rhodopseudomonas.
OX NCBI_TaxID=1076;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=CGA009 / ATCC BAA-98;
RX PubMed=14704707;
RA Laimmer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,
RA Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,
RA Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Peres C.,
RA Harrison F.H., Gibson J., Harwood C.S.;
RT "Complete genome sequence of the metabolically versatile
RT photosynthetic bacterium Rhodopseudomonas palustris.";
RL Nat. Biotechnol. 22:55-61(2004).
DR EMBL; BX572597; CAE26813.1;
SQ SEQUENCE 355 AA; 39283 MW; 7E37E937A2E431F0 CRC64;

Query Match 1.5%; Score 8; DB 2; Length 353;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 LSAVCRDL 362
DB 98 LSAVCRDL 105

RESULT 17
VE2_HPV65 STANDARD; PRT; 402 AA.

AC Q07851;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Regulatory protein E2.
GN Name=E2;
OS Human papillomavirus type 65.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=28312;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=93276568; PubMed=8389082;
RA Egawa K., Delius H., Matsukura T., Kawashima M., de Villiers E.M.;
RT "Two novel types of human papillomavirus, HPV 63 and HPV 65:
RT comparisons of their clinical and histological features and DNA
RT sequences to other HPV types.";
RL Virology 194:789-799(1993).
CC -1- FUNCTION: E2 regulates viral transcription and DNA replication. It
CC binds to the E2R5 response element (5'-ACNNNNNGGT-3') present in
CC multiple copies in the regulatory region. It can either activate
CC or repress transcription depending on E2R5's position with regards
CC to proximal promoter elements. Repression occurs by sterically
CC hindering the assembly of the transcription initiation complex.
CC The E1-E2 complex binds to the origin of DNA replication.
CC -1- SUBUNIT: Binds DNA as a dimer.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X70829; CAA50174.1; -
DR HSP; P06790; I14.
DR InterPro; IPR000427; E2_C.
DR InterPro; IPR001866; E2_N.
DR InterPro; IPR009021; Viral_DNA_bd.
DR Pfam; PF00511; PV_E2_C; 1.
DR Pfam; PF00508; PV_E2_N; 1.
DR ProDom; PD000672; E2_C; 1.
DR ProDom; PD000678; E2_N; 1.

KW Activator: DNA replication; DNA-binding; Early protein;
 KW Nuclear protein; Repressor; Trans-acting factor;
 KW Transcription regulation;
 SQ SEQUENCE 402 AA; 45552 MW; C7BA2B5325919FP4 CRC64;

Query Match 1.5%; Score 8; DB 1; Length 402;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 466 PGPGETPS 473
 DB 266 PGPGETPS 273

RESULT 18

ID Q702V2 PRELIMINARY; PRT; 404 AA.
 AC Q702V2;
 DT 05-JUL-2004 (TRMBLrel. 27, Created)
 DT 05-JUL-2004 (TRMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TRMBLrel. 27, Last annotation update)
 DE Putative outer membrane efflux protein.
 OS Yersinia enterocolitica.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 OX NCBI_TaxID=630;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=6471/76;
 RA Skurnik M., Lahtinen P., Brzezinska A.;
 RL Submitted (FEB-2004) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AJ626755; CAF25097.1; -.
 DR InterPro; IPR006143; HLYD.
 DR InterPro; IPR003423; OEP.
 DR InterPro; IPR010131; RND_outer_NodT.
 DR Pfam; PF02321; OEP; 1
 DR TIGRFAMs; TIGR01730; RND_mfp; 1.
 DR TIGRFAMs; TIGR01845; RND_outer_NodT; 1.
 SQ SEQUENCE 404 AA; 42501 MW; C7CB6686BE6571F0 CRC64;

Query Match 1.5%; Score 8; DB 2; Length 404;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 183 LETLYQSA 190
 DB 156 LETLYQSA 163

RESULT 19

ID CAF25097 PRELIMINARY; PRT; 404 AA.
 AC CAF25097;
 DT 02-MAR-2004 (TRMBLrel. 27, Created)
 DT 02-MAR-2004 (TRMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TRMBLrel. 27, Last annotation update)
 DE Putative outer membrane efflux protein.
 OS Yersinia enterocolitica.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 OX NCBI_TaxID=630;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=6471/76;
 RA Skurnik M., Lahtinen P., Brzezinska A.;
 RL "Temperature and growth phase regulate the transcription of the O-RT antigen gene cluster of Yersinia enterocolitica O:3.",
 RL submitted (FEB-2004) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AJ626755; CAF25097.1; -.
 KW Helicase.

SQ SEQUENCE 404 AA; 42501 MW; C7CB6686BE6571F0 CRC64;

Query Match 1.5%; Score 8; DB 2; Length 404;

Best Local Similarity 100.0%; Pred. No. 61;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 183 LETLYQSA 190
 DB 156 LETLYQSA 163

RESULT 20

ID Q9U133 PRELIMINARY; PRT; 628 AA.
 AC Q9U133;
 DT 01-OCT-2000 (TRMBLrel. 15, Created)
 DT 01-OCT-2000 (TRMBLrel. 15, Last sequence update)
 DT 05-JUL-2004 (TRMBLrel. 27, Last annotation update)
 DE Netrin 4 (Beta netrin).
 GN Name=Netn4;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ICR;
 RA MEDLINE=20400106; PubMed=10940631;
 RA Yin Y., Sanes J.R., Miner J.H.;
 RL "Identification and expression of mouse netrin-4.",
 RL Mech. Dev. 96:115-119(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RA MEDLINE=20493277; PubMed=11038171;
 RA Koch M., Muirrell J.R., Hunter D.D., Olson P.F., Jin W., Keene D.R.,
 RA Brunken W.J., Burgess R.B.;
 RL "A novel member of the netrin family, beta-netrin, shares homology with the beta chain of laminin. Identification, expression, and functional characterization.";
 RL J. Cell Biol. 151:221-234(2000).
 DR EMBL; AF268066; AA991404.1; -.
 DR EMBL; AF281278; AAG30823.1; -.
 DR HSSP; P02468; INPE.
 DR MGD; MGI:1888978; Ntn4.
 DR GO; GO:0016322; P:neuronal remodeling; IDA.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR008978; Gal_bind_like.
 DR InterPro; IPR002049; Laminin_EGF.
 DR InterPro; IPR008211; Laminin_N.
 DR InterPro; IPR001134; Netrin_C.
 DR InterPro; IPR008993; TIMP like.
 DR Pfam; PF00053; Laminin_EGF; 3.
 DR Pfam; PF00055; Laminin_N; 1.
 DR Pfam; PF01759; NTR; 1.
 DR PRINTS; PR00011; EGF_LAMININ.
 DR SMART; SM00643; C345C; 1.
 DR SMART; SM00180; EGF_Lam; 3.
 DR SMART; SMC0136; LAMNT; 1.
 DR PROSITE; PS00022; EGF_1; 2.
 DR PROSITE; PS01248; LAMININ_TYPE_EGF; 2.
 DR PROSITE; PS50189; NTR; 1.
 KW Laminin EGF-like domain.
 SQ SEQUENCE 628 AA; 69896 MW; 474F74745F236C7 CRC64;

Query Match

Best Local Similarity 100.0%; Pred. No. 92;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 LVRRLKX 10
 DB 224 LVRRLKX 231

RESULT 21

Q98FQ3

ID 098F09 PRELIMINARY; PRT; 686 AA.
AC 098F09;
DT 01-OCT-2001 (TRENBLrel. 18, Created)
DT 01-OCT-2001 (TRENBLrel. 18, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Mir3659 protein.
GN OrderedLocustNames=ml13659;
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneke T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Kimura T.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MAF303099;
RX MEDLINE=21082936; PubMed=11214974;
RA Kaneke T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Kimura T.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
Mesorhizobium loti (supplement).";
RL DNA Res. 7:381-406(2000).
CC -1- SIMILARITY: Contains 1 histidine kinase domain.
DR EMBL: AP003002; BAB50508.1; -.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR GO: GO:0016301; F:kinase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0000155; F:two-component sensor molecule activity; IEA.
DR GO: GO:0007600; F:sensory perception; IEA.
DR GO: GO:0000160; P:two-component signal transduction system (p. . .); IEA.
DR InterPro: IPR003594; ATPbind_ATPase.
DR InterPro: IPR004358; Bact_sens_pr_C.
DR InterPro: IPR011006; Chey_like.
DR InterPro: IPR003018; GAP.
DR InterPro: IPR005467; His_kinase.
DR InterPro: IPR003661; His_kin_N.
DR InterPro: IPR009082; His_kin_homodm.
DR InterPro: IPR001005; Myb_DNA_binding.
DR InterPro: IPR001610; PAC.
DR InterPro: IPR000014; PAS.
DR InterPro: IPR001789; Response_reg.
DR Pfam: PF01590; GAP. 1.
DR Pfam: PF02518; HATPase_C. 1.
DR Pfam: PF00512; HSKA. 1.
DR Pfam: PF00989; PAS. 1.
DR Pfam: PF00072; Response_reg. 1.
DR PRINTS: PR00344; BCTRLSENSOR.
DR PRODOM: PD000039; Response_reg. 1.
DR SMART: SM00065; GAP. 1.
DR SMART: SM00387; HATPase_C. 1.
DR SMART: SM00388; HSKA. 1.
DR SMART: SM00086; PAC. 1.
DR SMART: SM00091; PAS. 1.
DR SMART: SM00448; REC. 1.
DR TIGRFAMs: TIGR00229; sensory_box. 1.
DR PROSITE: PS50109; HIS_KIN. 1.
DR PROSITE: PS00037; MTB_1; UNKNOWN_1.

DR PROSITE: PS50112; PAS. 1.
DR PROSITE: PS50110; RESPONSE_REGULATORY. 1.
KW Complete proteome; kinase; phosphorylation; sensory transduction;
KW transferase.
SQ SEQUENCE 686 AA; 75044 MW; A50DD3932CC4FBE9 CRC64;
QY Query Match 1.5%; Score 8; DB 2; Length 686;
DB Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 347 LDVRSVLS 354
DB 669 LDVRSVLS 676
RESULT 22
ID 098K7 PRELIMINARY; PRT; 730 AA.
AC 098K7;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Hypothetical protein Atg25420.
GN Name=Atg25420;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., Vanaken S.E.,
RA Barnstead M.E., Mason T.M., Bowman C.L., Ranning C.M., Benito M.-I.,
RA Carreira A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,
RA Fraser C.M., Venter J.C.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Town C.D., Kaul S.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 2 WD repeats.
DR EMBL: AC006300; AAD20702.2; -.
DR PIR: B84648; B84648.
DR InterPro: IPR006595; CTIH_C.
DR InterPro: IPR006594; LISH_C.
DR InterPro: IPR001680; WD40.
DR InterPro: IPR011046; WD40_like.
DR Pfam: PF00400; WD40. 2.
DR SMART: SM00668; CTIH. 2.
DR SMART: SM00667; LISH. 2.
DR SMART: SM00320; WD40. 4.
DR PROSITE: PS50837; CTIH. 1.
DR PROSITE: PS50896; LISH. 2.
DR PROSITE: PS50082; WD_REPEATS_2. 1.
DR PROSITE: PS50294; WD_REPEATS_REGION. 1.
KW Hypothetical protein; Repeat; WD repeat.
SQ SEQUENCE 730 AA; 82003 MW; 16205CE1D3769F88 CRC64;
QY Query Match 1.5%; Score 8; DB 2; Length 730;
DB Best Local Similarity 100.0%; Pred. No. 1.e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 72 DILCILQ 79
DB 177 DILCILQ 184
RESULT 23
ID 0704C4 PRELIMINARY; PRT; 758 AA.
AC 0704C4;
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)

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DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE AGCP11203 (Fragment).
GN Name=agcG48900; ORFNames=ENSNANGS00000015760;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 4 WD repeats.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB0100864; EAI2424.1; -.
DR InterPro; IPR006575; RMD.
DR InterPro; IPR01680; WD40.
DR Pfam; PF00400; WD40.4.
DR PRINTS; PR00320; GPROTEINRPT.
DR PROSITE; PS50908; RMD; 1.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
DR PROSITE; PS50082; WD_REPEATS_2; 3.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
FT NON_TER 1
FT NON_TER 758
SQ SEQUENCE 758 AA; 84915 MW; D6F4CD3DBBEF0179 CRC64;

Query Match 1.5%; Score 8; DB 2; Length 758;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 352 VLISLAVC 359
Db 202 VLISLAVC 209

RESULT 24
Q74BT1 PRELIMINARY; PRT; 1047 AA.
ID Q74BT1
AC Q74BT1;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Fibronectin type III domain protein.
GN ORFNames=GSU1945;
OS Geobacter sulfurreducens.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
OC Geobacteraceae; Geobacter.
CX NCBI_TaxID=35554;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCA / ATCC 51573;
RX PubMed=14671304; DOI=10.1126/science.1088727;
RA Heideberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J.,
RA Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
RA Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
RA Davidson T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
RA Weidman J., Kouri H.M., Feldblyum T.V., Uitterlind T.R.,
RA Van Aken S.E., Lovley D.R., Fraser C.M.;
RA "Genome of Geobacter sulfurreducens: metal reduction in subsurface
RT environments.";
RL Science 302:1967-1969(2003).
DR EMBL; AE017180; AAR35321.1; -.
DR TIGR; GSU1945; -.
DR InterPro; IPR002105; Dokerin_1.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR000601; PKD.

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DR Pfam; PF00041; FN3; 1.
DR PROSITE; PS50853; FN3; 1.
SQ SEQUENCE 1047 AA; 106532 MW; 3C491BA2DAB493C0 CRC64;

Query Match 1.5%; Score 8; DB 2; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 ANDALIVL 202
Db 987 ANDALIVL 994

RESULT 25
AAR35321 PRELIMINARY; PRT; 1047 AA.
ID AAR35321
AC AAR35321;
DT 02-MAR-2004 (TREMBLrel. 27, Created)
DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)
DE Fibronectin type III domain protein.
GN GSU1945.
OS Geobacter sulfurreducens.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
OC Geobacteraceae; Geobacter.
CX NCBI_TaxID=35554;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCA / ATCC 51573;
RX PubMed=14671304;
RA Heideberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J.,
RA Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
RA Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
RA Davidson T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
RA Weidman J., Kouri H.M., Feldblyum T.V., Uitterlind T.R.,
RA Van Aken S.E., Lovley D.R., Fraser C.M.;
RA "Genome of Geobacter sulfurreducens: metal reduction in subsurface
RT environments.";
RL Science 302:1967-1969(2003).
DR EMBL; AE017214; AAR35321.1; -.
DR TIGR; GSU1945; -.
SQ SEQUENCE 1047 AA; 106532 MW; 3C491BA2DAB493C0 CRC64;

Query Match 1.5%; Score 8; DB 2; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 ANDALIVL 202
Db 987 ANDALIVL 994

RESULT 26
Q8TU06 PRELIMINARY; PRT; 67 AA.
ID Q8TU06
AC Q8TU06;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Helix-turn-helix family protein.
GN OrderedLocustNames=MA3984;
OS Methanococcus marisnigri.
OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
CX NCBI_TaxID=2214;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=11932238; DOI=10.1101/gr.223902;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA Fitzhugh W., Calvo S., Engels R., Smirnov S., Alnoor D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., Deatellano K., Johnson R.,

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RA Linton L., McEwan P., McKernan K., Talamas J., Tittrell A., Ye W.,
 RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
 RA Hedderich R., Ingram-Smith C., Kuettnner H.C., Krzycki J.A.,
 RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
 RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
 RA Ferry J.G., Jarell K.F., Jung H., Macario A.J.L., Paulsen I.T.,
 RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Zander E.,
 RA Metcalf W.W., Birren B.,
 RT "The genome of *Methanoscarius aceti* reveals extensive metabolic
 RT and physiological diversity.";
 RL Genome Res. 12:532-542 (2002).
 DR EMBL: AEO1110; F:DNA binding; IEA.
 DR GO: GO:0003677; F:DNA binding; IEA.
 DR InterPro: IPR001387; HTH_3.
 DR InterPro: IPR010982; Lambda_like_DNA.
 DR Pfam: PF01381; HTH_3; 1.
 DR SMART: SMO0530; HTH_XRE; 1.
 DR PROSITE: PS00943; HTH_CROCI; 1.
 KM Complete proteome.
 SQ SEQUENCE 67 AA; 7746 MW; C22489D51A0B9DD6 CRC64;

Query Match 1.3%; Score 7; DB 2; Length 67;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 303 KLSRLFX 309
 DB 47 KLSRLFX 53

RESULT 27
 O8SNT0
 ID O8SNT0 PRELIMINARY; PRT; 67 AA.
 AC O8SNT0;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE MHC class II antigen (Fragment).
 GN Name:HagG-DRB;
 OS Haploleum griseus griseus.
 OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Strepsirrhini; Lemnidae; Haploleum.
 OX NCBI_TaxID=122219;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Go Y., Satia Y., Kawamoto Y., Rakotoarisoa G., Randrianjafo A.,
 RA Koyama N., Hirai H.,
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB078293; BAB8506.1;
 DR GO: GO:0016021; C:Integral to membrane; IEA.
 DR GO: GO:0045012; F:MHC class II receptor activity; IEA.
 DR GO: GO:0019884; P:antigen presentation, exogenous antigen; IEA.
 DR GO: GO:0019886; P:antigen processing, exogenous antigen via M. . .; IEA.
 DR GO: GO:0006955; P:immune response; IEA.
 DR InterPro: IPR000353; MHC_II_beta.
 DR Pfam: PF00969; MHC_II_beta; 1.
 DR ProDom: PD000328; MHC_II_beta; 1.
 KW Glycoprotein; MHC II; Transmembrane.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 67 AA; 8128 MW; B0D7F590721E89F9 CRC64;

Query Match 1.3%; Score 7; DB 2; Length 67;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 RVRLIKR 10
 DB 2 RVRLIKR 8

RESULT 28
 Q7R6Q1

ID Q7R6Q1 PRELIMINARY; PRT; 80 AA.
 AC Q7R6Q1;
 DT 01-MAR-2004 (TREMBlrel. 26, Created)
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE GLP 170 54038 54280.
 OS Giardia lamblia ATCC 50803.
 OC Eukaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia.
 OX NCBI_TaxID=184922;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MB C6;
 RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
 RA Olsen G.J., Sogin M.L.;
 RT "Direct sequence of the Giardia lamblia genome.";
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 CC -! CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL: AACB01000001; EAA42946.1; -
 DR InterPro: IPR002453; Beta_tubulin.
 DR PROSITE: PS00228; TUBULIN_E_AUTOREG; UNKNOWN 1.
 SQ SEQUENCE 80 AA; 9004 MW; C1CCH76CB4ACAB8E CRC64;

Query Match 1.3%; Score 7; DB 2; Length 80;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 28 SHRLSL 34
 DB 10 SHRLSL 16

RESULT 29
 O76H60
 ID O76H60 PRELIMINARY; PRT; 80 AA.
 AC O76H60;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE ORF46.
 GN Name=orf46;
 OS Salmonella typhimurium bacteriophage ST104.
 OC Viruses.
 OX NCBI_TaxID=221029;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA PubMed=15071057;
 RA Tanaka K., Nishimori K., Makino S., Nishimori T., Kanno T.,
 RA Ishihara R., Samehima T., Akiba M., Nakazawa M., Yokomizo Y.,
 RA Uchida I.;
 RT "Molecular characterization of a prophage of *Salmonella enterica*
 RT serotype Typhimurium DT104.";
 RL J. Clin. Microbiol. 42:1807-1812 (2004).
 DR EMBL: AB102868; BAD15208.1; 4715B951676D57 CRC64;
 SQ SEQUENCE 80 AA; 8565 MW; 4715B951676D57 CRC64;

Query Match 1.3%; Score 7; DB 2; Length 80;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 307 LKRDQIV 313
 DB 44 LKRDQIV 50

RESULT 30
 BAD15208
 ID BAD15208 PRELIMINARY; PRT; 80 AA.
 AC BAD15208;
 DT 14-APR-2004 (TREMBlrel. 27, Created)
 DT 14-APR-2004 (TREMBlrel. 27, Last sequence update)
 DT 14-APR-2004 (TREMBlrel. 27, Last annotation update)

DE ORF46.
 GN ORF46.
 OS Salmonella typhimurium bacteriophage ST104.
 OC Viruses.
 RX NCBI_TaxID=221029;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tanaka K., Nishimori K., Makino S., Nishimori T., Kanno T.,
 RA Ishihara R., Sameshima T., Akiba M., Nakazawa M., Yokomizo Y.,
 RA Uchida I.,
 RT "Molecular Characterization of a Prophage of Salmonella enterica
 RT Serotype Typhimurium DT104,"
 RL J. Clin. Microbiol. 42:1807-1812(2004).
 DR EMBL: AB102868; BAD15208.1; -
 SQ SEQUENCE 80 AA; 8565 MW; 4715HB9516766D57 CRC64;

Query Match 1.3%; Score 7; DB 2; Length 80;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 307 LFKDOLV 313
 DB 44 LFKDOLV 50

RESULT 31

07P7A6 PRELIMINARY; PRT; 82 AA.
 AC 07P7A6.
 DT 01-MAR-2004 (TRENBLREL. 26, Created)
 DT 01-MAR-2004 (TRENBLREL. 26, Last sequence update)
 DE Hypothetical protein.
 GN Name=FV1647;
 OS Fusobacterium nucleatum subsp. vincentii ATCC 49256.
 OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;
 CC Fusobacterium.
 CX NCBI_TaxID=209882;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 49256;
 RA Karpatral V., Ivanova N., Anderson I., Reznik G., Bhattacharya A.,
 RA Gardner W.L., Mikhailova N., Larsen N., D'Souza M., Walunas T.,
 RA Haecklorn R., Overbeek R., Kyriides N.,
 RL Submitted (JAN-2003) to the EMBL/Genbank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL: AABR0100019; EAA24690.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 82 AA; 8526 MW; 8ED40FPADB00D6B1 CRC64;

Query Match 1.3%; Score 7; DB 2; Length 82;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 GSSATLT 251
 DB 24 GSSATLT 30

RESULT 32

P74781 PRELIMINARY; PRT; 84 AA.
 AC P74781.
 DT 01-FEB-1997 (TRENBLREL. 02, Created)
 DT 01-FEB-1997 (TRENBLREL. 02, Last sequence update)
 DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
 DE Ssl1707 protein.
 GN OrderedLocustNames=ssl1707;
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 CX NCBI_TaxID=1148;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PCC6803;
 RX MEDLINE=97061201; PubMed=8905231;
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hiroseawa M., Sugita M., Saito T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Nanno K., Okumura S.,
 RA Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
 RA Tabata S.,
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions,"
 RL DNA Res. 3:109-136(1996).
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96127529; PubMed=8590279;
 RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
 RA Sugita M., Tabata S.,
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
 RT region from map positions 64% to 92% of the genome,"
 RL DNA Res. 2:153-166(1995).
 DR EMBL: D64006; BAA10859.1; -
 DR F1R; S76012; S76012.
 DR HSP; C9X078; 1JDO.
 DR GO: GO:0008151; P:cell growth and/or maintenance; IEA.
 DR InterPro: IPR001455; SIRA_like.
 KW Complete proteome.
 SQ SEQUENCE 84 AA; 9257 MW; DA02DA1FF39DBC97 CRC64;

Query Match 1.3%; Score 7; DB 2; Length 84;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 QVPHSL 184
 DB 49 QVPHSL 55

RESULT 33

09G218 PRELIMINARY; PRT; 89 AA.
 AC 09G218.
 DT 01-MAR-2001 (TRENBLREL. 16, Created)
 DT 01-MAR-2001 (TRENBLREL. 16, Last sequence update)
 DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
 DE Cytochrome oxidase II (Fragment).
 OS Eremococcus queenslandensis.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pelegrina;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Chalcidoidea;
 OC Aphelinidae; Aphelininae; Eremocerus.
 CX NCBI_TaxID=131217;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA De Barro P.J., Driver F., Naumann I.D., Schmidt S., Clarke G.M.,
 RA Curran U.,
 RT "Descriptions of three species of Eremocerus Halteman (Hymenoptera:
 RT Aphelinidae) parasitising Bemisia tabaci (Gennadius) (Hemiptera:
 RT Aleyrodidae) and Trialeurodes vaporariorum (Westwood) (Hemiptera:
 RT Aleyrodidae) in Australia based on morphological and molecular data,"
 RL Aust. J. Entomol. 39:259-265(2000).
 CC -!- FUNCTION: Cytochrome c oxidase is the component of the respiratory
 CC chain that catalyzes the reduction of oxygen to water. Subunits 1-
 CC 3 form the functional core of the enzyme complex. Subunit 2
 CC transfers the electrons from cytochrome c via its binuclear copper
 CC A center to the bimetallic center of the catalytic subunit 1 (By
 CC similarity).
 CC -!- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome
 CC c + 2 H(2)O.
 CC -!- COFACTOR: Copper A (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane (By similarity).

-1- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.
 DR EMBL: AF275294; AAG25098.1; -
 DR EMBL: AF275287; AAG25091.1; -
 DR EMBL: AF275288; AAG25092.1; -
 DR EMBL: AF275289; AAG25093.1; -
 DR EMBL: AF275290; AAG25094.1; -
 DR EMBL: AF275291; AAG25095.1; -
 DR EMBL: AF275292; AAG25096.1; -
 DR EMBL: AF275293; AAG25097.1; -
 DR GO: 0016020; C:membrane; IEA.
 DR GO: 0005739; C:mitochondrion; IEA.
 DR GO: 0005507; F:copper ion binding; IEA.
 DR GO: 0004129; F:cytochrome-c oxidase activity; IEA.
 DR GO: 0006118; F:electron transport; IEA.
 DR InterPro: IPR001505; Copper_CuA.
 DR InterPro: IPR008972; Cupredoxin.
 DR Pfam: PF00116; COX2; 1.
 DR PRINTS: PR01166; CYCOXIDASEII.
 DR ProDom: PD000131; Copper_CuA; 1.
 DR Copper; Electron transport; Inner membrane; Mitochondrion;
 KW Oxidoreductase; Respiratory chain; Transmembrane; Transport.
 FT NON_TER 1
 FT NON_TER 89
 SQ SEQUENCE 89 AA; 10424 MW; 056B831A018474A2 CRC64;
 Query Match 1.3%; Score 7; DB 2; Length 89;
 Best Local Similarity 100.0%; Pred.No.1.7e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 343 IFRLLDV 349
 Db 26 IFRLLDV 32
 RESULT 34
 Q9G9G6 PRELIMINARY; PRT; 89 AA.
 AC Q9G9G6;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Cytochrome oxidase II (Fragment).
 OS Eremocerus queenslandensis.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Chalcidoidea;
 OC Aphelinidae; Aphelininae; Eremocerus.
 OX NCBI_TaxID=111217;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA De Barro P.J., Driver F., Naumann I.D., Schmidt S., Clarke G.M.,
 RT Curran J.;
 RT "Descriptions of three species of Eremocerus Haldeman (Hymenoptera:
 RT Aphelinidae) parasitising Bemisia tabaci (Gennadius) (Hemiptera:
 RT Aleyrodidae) and Trialeurodes vaporariorum (Westwood) (Hemiptera:
 RT Aleyrodidae) in Australia based on morphological and molecular data.";
 RL Aust. J. Entomol. 39:259-269(2000).
 CC -1- FUNCTION: Cytochrome c oxidase is the component of the respiratory
 CC chain that catalyzes the reduction of oxygen to water. Subunits 1-
 CC 3 form the functional core of the enzyme complex. Subunit 2
 CC transfers the electrons from cytochrome c via its binuclear copper
 CC A center to the bimetallic center of the catalytic subunit 1 (By
 CC similarity).
 CC -1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferriycyclochrome
 CC c + 2 H(2)O.
 CC -1- COFACTOR: Copper A (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane (By similarity).
 CC -1- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.
 DR EMBL: AF275295; AAG25099.1; -
 DR GO: 0016020; C:membrane; IEA.
 DR GO: 0005739; C:mitochondrion; IEA.

DR GO: 0005507; F:copper ion binding; IEA.
 DR GO: 0004129; F:cytochrome-c oxidase activity; IEA.
 DR GO: 0006118; F:electron transport; IEA.
 DR InterPro: IPR001505; Copper_CuA.
 DR InterPro: IPR008972; Cupredoxin.
 DR Pfam: PF00116; COX2; 1.
 DR PRINTS: PR01166; CYCOXIDASEII.
 DR ProDom: PD000131; Copper_CuA; 1.
 DR Copper; Electron transport; Inner membrane; Mitochondrion;
 KW Oxidoreductase; Respiratory chain; Transmembrane; Transport.
 FT NON_TER 1
 FT NON_TER 89
 SQ SEQUENCE 89 AA; 10442 MW; E12A831D6B29B3C8 CRC64;
 Query Match 1.3%; Score 7; DB 2; Length 89;
 Best Local Similarity 100.0%; Pred.No.1.7e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 343 IFRLLDV 349
 Db 26 IFRLLDV 32
 RESULT 35
 Q6GV22 PRELIMINARY; PRT; 91 AA.
 AC Q6GV22;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Myeloid differentiation factor 88 (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Kuminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Werling D.;
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: A634627; AAT48485.1; -
 DR InterPro: IPR00157; TIR.
 DR PROSITE: PS50104; TIR; 1.
 FT NON_TER 1
 FT NON_TER 91
 SQ SEQUENCE 91 AA; 10658 MW; 37E1C22DB6DBE463 CRC64;
 Query Match 1.3%; Score 7; DB 2; Length 91;
 Best Local Similarity 100.0%; Pred.No.1.7e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 219 AKALSM 225
 Db 85 AKALSM 91
 RESULT 36
 Q9ZVS3 PRELIMINARY; PRT; 91 AA.
 AC Q9ZVS3;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE F15K9.18.
 GN Name=F15K9.18;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Vysotskaya V.S., Schwartz J.R., Toriumi M., Yu G., Li J., Liu S.,

RA Kremenetskaia I., Luos J., Araujo R., Buehler E., Conway A.B.,
 RA Dwyer K., Feng J., Kim C., Li Y., Shinn P., Sun H., Davis R.W.,
 RA Ecker J.R., Federspiel N.A., Theologis A.,
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: ACC05278; AAC72126.1; -
 DR PIR: E86163; E86163.
 SQ SEQUENCE 91 AA; 10600 MW; EBCB45170E6D1CA4 CRC64;

Query Match 1.3%; Score 7; DB 2; Length 91;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 316 LLAFTRO 322
 DB 80 LLAFTRO 86

RESULT 37

O89TW2 PRELIMINARY; PRT; 91 AA.
 ID O89TW2
 AC O89TW2
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Bsl1884 protein.
 GN OrderedLocustNames=bsl1884;
 OS Bradyrhizobium japonicum.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Bradyrhizobiaceae;
 OC NCB1_TaxID=375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=USDA110;
 RX MEDLINE=22484998; PubMed=12597275;
 RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
 RA Sasamoto S., Watanabe A., Ideawa K., Iriyuchi M., Kawashima K.,
 RA Kohara M., Matsumoto M., Shimo S., Tsuruoka H., Wada T., Yamada M.,
 RA Tabata S.,
 RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
 RT Bradyrhizobium japonicum USDA110."
 RL DNA Res. 9:189-197(2002).
 DR EMBL: AP005941; BAC67419.1; -
 DR InterPro: IPR009056; Cytochrome_C.
 KW Complete proteome.
 SQ SEQUENCE 91 AA; 9786 MW; B36FA66807EAA53 CRC64;

Query Match 1.3%; Score 7; DB 2; Length 91;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 439 LPPGIIIG 445
 DB 67 LPPGIIIG 73

RESULT 38

O6YWB6 PRELIMINARY; PRT; 92 AA.
 ID O6YWB6
 AC O6YWB6
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 01-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Hypothetical protein P0501E09.15 (Hypothetical protein
 DE P0584E12.42).
 GN Name=P0501E09.15; Synonyms=P0584E12.42;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriactoidae; Oryzaceae; Oryza.
 OC NCB1_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Hattori M., Sakaki Y., Katayose Y.,
 RA Sasaki T., Matsumoto T., Hattori M., Sakaki Y., Katayose Y.,

RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Sasaki T., Matsumoto T., Hattori M., Sakaki Y., Katayose Y.,
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AP005787; BAD17570.1; -
 DR EMBL: AP005591; BAD17403.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 92 AA; 9772 MW; 085A4B6C65893581 CRC64;

Query Match 1.3%; Score 7; DB 2; Length 92;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 509 PSRGPRPT 515
 DB 7 PSRGPRPT 13

RESULT 39

BAD17403 PRELIMINARY; PRT; 92 AA.
 ID BAD17403
 AC BAD17403
 DT 10-MAY-2004 (TREMBlrel. 27, Created)
 DT 10-MAY-2004 (TREMBlrel. 27, Last sequence update)
 DT 10-MAY-2004 (TREMBlrel. 27, Last annotation update)
 DE Hypothetical protein P0584E12.42.
 GN P0584E12.42
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriactoidae; Oryzaceae; Oryza; Oryza sativa.
 OC NCB1_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Katayose Y.,
 RT "Oryza sativa nipponbare (Ga3) genomic DNA, chromosome 9, PAC
 RT clone: P0584E12."
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AP005591; BAD17403.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 92 AA; 9772 MW; 085A4B6C65893581 CRC64;

Query Match 1.3%; Score 7; DB 2; Length 92;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 509 PSRGPRPT 515
 DB 7 PSRGPRPT 13

RESULT 40

BAD17570 PRELIMINARY; PRT; 92 AA.
 ID BAD17570
 AC BAD17570
 DT 10-MAY-2004 (TREMBlrel. 27, Created)
 DT 10-MAY-2004 (TREMBlrel. 27, Last sequence update)
 DT 10-MAY-2004 (TREMBlrel. 27, Last annotation update)
 DE Hypothetical protein P0501E09.15.
 GN P0501E09.15
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriactoidae; Oryzaceae; Oryza; Oryza sativa.
 OC NCB1_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Hattori M., Sakaki Y., Katayose Y.,
 RA Sasaki T., Matsumoto T., Hattori M., Sakaki Y., Katayose Y.,
 RT "Oryza sativa nipponbare (Ga3) genomic DNA, chromosome 9, PAC
 RT clone: P0501E09."

RL Submitted (SFP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF005787; BADI7570.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 92 AA; 9772 MW; 085A4BBC65893581 CRC64;

Query Match
 Best Local Similarity 100.0%; Score 7; DB 2; Length 92;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 509 PSRGRPT 515
 Db 7 PSRGRPT 13

RESULT 41

Q9V0B7 PRELIMINARY; PRT; 96 AA.
 AC Q9V0B7;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocustNames=PYRAB09730; ORFNames=PAB7218;
 OS Pyrococcus abyssi.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 NCBI_TaxID=29292;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GES / Orsay;
 RX MEDLINE=22511545; PubMed=12622808;
 RA Cohen G.N., Barde V., Flament D., Galperin M., Heilig R., Lecomte O.,
 RA Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C.,
 RA Van der Oost J., Weisenbach J., Zivanovic Y., Forterre P.;
 RT "An integrated analysis of the genome of the hyperthermophilic
 RT archaeon Pyrococcus abyssi."
 RL Mol. Microbiol. 47:1495-1512(2003).
 DR EMBL: AJ248285; CAB49787.1; -.
 DR PIR: B75134;
 DR InterPro: IPR002716; P1LT_N.
 DR Pfam: PF01850; PIN_1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 96 AA; 11308 MW; 88A44EBB5A352D6 CRC64;

Query Match
 Best Local Similarity 100.0%; Score 7; DB 2; Length 96;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 196 NDALIVL 202
 Db 63 NDALIVL 69

RESULT 42

O81E48 PRELIMINARY; PRT; 105 AA.
 AC O81E48;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE 5-methylcytosine-specific restriction enzyme A (EC 3.1.21.-).
 GN OSFNames=BC1144;
 OS Bacillus cereus (strain ATCC 14579 / DSM 31).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 NCBI_TaxID=226900;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
 RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
 RA Kapatarel V., Bhattacharya A., Reznik G., Mikhailova N., Lapidus A.,
 RA Chu L., Mazur M., Goltzman E., Larsen N., D'Souza M., Walunas T.,
 RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
 RA Overbeek R., Kyrpides N.C.;

RT "Genome sequence of Bacillus cereus and comparative analysis with
 RT Bacillus anthracis."
 RL Nature 423:87-91(2003).
 DR EMBL: AE017004; AAP0911.1; -.
 DR GO:0016787; F:hydrolase activity; IEA.
 KW Hydrolase.
 SQ SEQUENCE 105 AA; 11860 MW; 642040A37CFA113 CRC64;

Query Match
 Best Local Similarity 100.0%; Score 7; DB 2; Length 105;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 LFTASND 368
 Db 8 LFTASND 14

RESULT 43

O54878 PRELIMINARY; PRT; 110 AA.
 AC O54878;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Streptococcus pneumoniae.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 NCBI_TaxID=1313;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SP1000; TRANSPOSON=Th5252;
 RX MEDLINE=94327488; PubMed=8051031;
 RA Kilic A.O., Vijayakumar M.N., al-Khalidi S.F.;
 RT "Identification and nucleotide sequence analysis of a transfer-related
 RT region in the streptococcal conjugative transposon Th5252."
 RL J. Bacteriol. 176:5145-5150(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SP1000; TRANSPOSON=Th5252;
 RA Vijayakumar M.N.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U29324; AAC98429.1; -.
 DR PIR: B55863; B55863.
 KW Hypothetical protein.
 SQ SEQUENCE 110 AA; 13053 MW; 3836A80B2F6D6B96 CRC64;

Query Match
 Best Local Similarity 100.0%; Score 7; DB 2; Length 110;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 YKDPPLTG 58
 Db 21 YKDPPLTG 27

RESULT 44

O8MT79 PRELIMINARY; PRT; 111 AA.
 AC O8MT79;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Drosophila melanogaster (Fruit fly).
 GN Name=1(1)G0269;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydrioides; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;

Stapleton M., Brokstein P., Hong J., Agbayani A., Carlson J.,
 RA Campe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Munnell C.J., Nunoo J., Pacleb J., Parasas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Ceiniker S.,
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY118321; AAM48350.1; -
 DR FlyBase: FBgn029067; 1(1)G0269.
 DR InterPro: IPR004274; NIF.
 DR Pfam: PF03031; NIF: 1.
 DR SMART: SM00577; CPDC: 1.
 DR SEQUENCE 111 AA; 12851 MW; B6B37648AA07E524 CRC64;

Query Match 1.3%; Score 7; DB 2; Length 111;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 348 DRSVLS 354
 DB 96 DRSVLS 102

RESULT 45

09ANA6 PRELIMINARY; PRT: 112 AA.
 AC 09ANA6;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE ID385.
 GN Name=Id385;
 OS Bradyrhizobium japonicum.
 CC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 CC Bradyrhizobiaceae; Bradyrhizobium.
 OX NCBI_TaxID=375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1105PC4;
 RX MEDLINE=21101824; PubMed=11157954;
 RA Gottfert M., Rothlisberger S., Kundig C., Beck C., Marty R.,
 RA Hennecke H.,
 RT "Potential symbiosis-specific genes uncovered by sequencing a 410-kb
 RT DNA region of the Bradyrhizobium japonicum chromosome."
 RL J. Bacteriol. 183:1405-1412 (2001).
 DR EMBL: AF322012; AAG60867.1; -
 DR InterPro: IPR009056; Cytochrome C
 DR SEQUENCE 112 AA; 12069 MW; 98E2D9BF6ED5366 CRC64;

Query Match 1.3%; Score 7; DB 2; Length 112;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 439 LPPGIG 445
 DB 88 LPPGIG 94

RESULT 46

08HAE8 PRELIMINARY; PRT: 118 AA.
 AC 08HAE8;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Orf-118.
 GN Name=orf-118;
 OS Bacteriophage ST64T
 CC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae.
 OX NCBI_TaxID=173443;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22638307; PubMed=12754248;

Mucilawa P.T., Schmieger H., Tucker C.P., Heuzenroeder M.W.,
 RA "Genomic structure of the Salmonella enterica serovar Typhimurium DT
 RT 64 bacteriophage ST64T: evidence for modular genetic architecture."
 RL J. Bacteriol. 185:3473-3475 (2003).
 DR EMBL: AY052766; AAL15520.1; -
 DR SEQUENCE 118 AA; 12875 MW; AE45EFC6C6A8C0C8 CRC64;

Query Match 1.3%; Score 7; DB 2; Length 118;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 307 LFKDQV 313
 DB 82 LFKDQV 88

RESULT 47

08CU33 PRELIMINARY; PRT: 120 AA.
 AC 08CU33;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Hypothetical.
 GN OrderedlocusNames=y2310;
 OS Yersinia pestis.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Yersinia.
 OX NCBI_TaxID=632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KIMS / Biovar Mediaevalis;
 RX MEDLINE=22137863; PubMed=12142430;
 RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
 RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C., V.,
 RA Peterson J.D., Lindler L.B., Brubaker R.R., Plano G.V.,
 RA Straley S.C., McDonough K.A., Niles W.L., Watson J.S., Blattner F.R.,
 RA Perry R.D.,
 RT "Genome sequence of Yersinia pestis KIM."
 RL J. Bacteriol. 184:4601-4611 (2002).
 DR EMBL: AE013833; AAM95869.1; -
 DR GO: GO:0003824; P: catalytic activity, IRA.
 DR GO: GO:0006725; P: aromatic compound metabolism, IRA.
 DR InterPro: IPR003779; CMD.
 DR Pfam: PF02627; CMD; 1.
 DR Hypothetical protein.
 DR SEQUENCE 120 AA; 13320 MW; 7DFF4DADA5DE5A56 CRC64;

Query Match 1.3%; Score 7; DB 2; Length 120;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 LRSHRL 32
 DB 72 LRSHRL 78

RESULT 48

08CU9 PRELIMINARY; PRT: 123 AA.
 AC 08CU9;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Mus musculus 15 days embryo brain cDNA, RIKEN full-length enriched
 DE library, clone:G630024G08 product: hypothetical protein, full insert
 DE sequence.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Brain;
 RX MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RA The FANTOM Consortium;
 RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Smiti N., Ishii Y., Nakamura S., Hazama M., Nishimura T., Harada A.,
 RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RA Aichi U., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imetani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ono M., Onose N., Sano H.,
 RA Saito K., Satoh H., Sakai C., Sakai K., Sakazume N., Sato H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi P., Takaku-Akahira S., Takada Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: ACO90243; BAC41145.1;
 DR GO: GO:0016020; Cimetidine; IEA.
 DR InterPro: IPR005052; Lectin leg.
 DR Pfam: PF03388; Lectin_leg-Ilike; 1.
 DR Hypothetical protein.
 DR KMW
 SQ SEQUENCE 123 AA; 13394 MW; DF3FCB1E921895B CRC64;

Query Match 1.3%; Score 7; DB 2; Length 123;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 430 HRPFPs 436
 DB 113 HRPFPs 119

RESULT 49
 ID Q81RB0 PRELIMINARY; PRT; 125 AA.
 AC Q81RB0; Q6H213; Q6KTH3;
 DT 01-JUN-2003 (TREMblrel. 24, Created)
 DT 01-JUN-2003 (TREMblrel. 24, Last sequence update)
 DT 01-OCT-2004 (TREMblrel. 28, Last annotation update)
 DE Conserved domain protein.
 GN Ordered locus names=BAC2140, BAS1992; ORFNames=GBAA2140;
 OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1392;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Ames / isolate Porton;
 RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
 RA Read T.D., Peterson S.N., Tourasse N.J., Ballile L.W., Paulsen I.T.,
 RA Nelson K.E., Tetteh N.H., Fouts D.E., Eisen J.A., Gill S.R.,
 RA Holtzapple E.K., Okstad O.A., Helgason E., Ristone J., Wu M.,
 RA Kolonay J.F., Beaman M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
 RA DeBoy R.T., Madpu R., Dougherty S.C., Durkin A.S., Haft D.H.,
 RA Nelson W.C., Peterson U.D., Pop M., Khouri H.M., Radune D.,
 RA Benson J.C., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
 RA Berry K.J., Plant R.D., Wolf A.M., Watkins K.L., Newman W.C.,
 RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
 RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,
 RA Hanna P.C., Kolstoe A.-B., Fraser C.M.,
 RT "The genome sequence of *Bacillus anthracis* Ames and comparison to closely related bacteria.";
 RL Nature 423:81-86(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Ames / isolate 0581;
 RA Ravel J., Basko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
 RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
 RA Frazer C.M.;
 RT "Bacillus anthracis comparative genomics";
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sterner;
 RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
 RA Hitchcock P., Jackson P., Kelm P., Longmire J., Lucas S., Okinaka R.,
 RA Richardson P., Rubin E., Tice H.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AE017030; AAP26024.1;
 DR EMBL: AE017334; AAT31258.2;
 DR EMBL: AE017225; AAT54306.1;
 DR TIGR: BA2140;
 DR InterPro: IPR002110; ANK.
 DR PRINTS: PRO1415; ANKYRIN.
 SQ SEQUENCE 125 AA; 14820 MW; FA4489EE44B9B35 CRC64;

Query Match 1.3%; Score 7; DB 2; Length 125;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 68 IVSGDLI 74
 DB 9 IVSGDLI 15
 RESULT 50
 ID AAT31258 PRELIMINARY; PRT; 125 AA.
 AC AAT31258;
 DT 01-JUN-2004 (TREMblrel. 27, Created)
 DT 01-JUN-2004 (TREMblrel. 27, Last sequence update)
 DT 01-JUN-2004 (TREMblrel. 27, Last annotation update)
 DE Conserved domain protein.
 GN GBAA2140.
 OS *Bacillus anthracis* str. Ames 0581.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 OC Bacillus cereus group; Bacillus anthracis.
 OX NCBI_TaxID=261594;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Ames 0581;
 RA Ravel J., Rasko D., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
 RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S., Fraser C.M.;
 RT "Bacillus anthracis comparative genomics";
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE017314; AAT31258.2; -
 SQ SEQUENCE 125 AA; 14820 MW; FA4489EB45E8935 CRC64;

Query Match 1.3%; Score 7; DB 2; Length 125;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 IVSGDLI 74
 Db 9 IVSGDLI 15

RESULT 51
 SSB2 STRAS STANDARD; PRT; 131 AA.
 ID SSB2 STRAS
 AC Q8E7H6;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE Single-strand binding protein 2 (SSB 2) (Helix-destabilizing protein 2).
 GN Name=ssb2; OrderedLocNames=gbs0178;
 OS Streptococcus agalactiae (serotype III).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=216495;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MEM316 / Serotype III;
 RA MEDLINE=22242508; PubMed=12354221;
 RA Glaser P., Rusnok C., Buchrieser C., Chevallier F., Frangoul L.,
 RA Masdek T., Zouine M., Couve E., Lallouf L., Poyart C., Trieu-Cuot P.,
 RA Kunst F.;
 RT "Genome sequence of Streptococcus agalactiae, a pathogen causing
 RT invasive neonatal disease.";
 RL Mol. Microbiol. 45:1499-1513(2002).
 CC -1- FUNCTION: This protein is essential for replication of the
 CC chromosome. It is also involved in DNA recombination and repair
 CC (by similarity).
 CC -1- SIMILARITY: Contains 1 SSB domain.
 CC -----
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 CC -----
 CC EMBL; AL766844; CAD45823.1; -
 DR HSSP; P02339; 1EYG.
 DR Sagalistic; gbs0178; -
 DR InterPro; IPR008994; Nucleic_acid_OB.
 DR InterPro; IPR00424; SSB_protein.
 DR InterPro; IPR010913; SS_binding.
 DR Pfam; PF00436; SSB; 1.
 DR TIGRFAMs; TIGR00621; ssb; 1.
 DR PROSITE; PS50935; SSB; 1.
 DR Complete proteome; DNA repair; DNA replication; DNA-binding.
 FT DOMAIN 1 103 SSB.
 SQ SEQUENCE 131 AA; 14791 MW; 447B06B0420411DD CRC64;

Query Match 1.3%; Score 7; DB 1; Length 131;

Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 ETLASYG 67
 Db 59 ETLASYG 65

RESULT 52
 SSB2 STRAS STANDARD; PRT; 131 AA.
 ID SSB2 STRAS
 AC Q8E7H6;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Single-strand binding protein 2 (SSB 2) (Helix-destabilizing protein 2).
 GN Name=ssb2; OrderedLocNames=SAG0180;
 OS Streptococcus agalactiae (serotype V).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=216466;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=2603 V/R / Serotype V;
 RA MEDLINE=22222988; PubMed=12200547; DOI=10.1073/pnas.182380799;
 RA Tettelin H., Maignani V., Cieslewicz M.J., Eisen J.A., Peterson S.N.,
 RA Wessels M.R., Paulsen I.T., Nelson K.E., Margalit I., Read T.D.,
 RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
 RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
 RA Radune D., Federova N.B., Scanlan D., Khouli H.M., Mulligan S.,
 RA Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
 RA Tacchini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Malone D.,
 RA Rinaldo D., Rappelli R., Telford J.L., Kasper D.L., Grandi G.,
 RA Frazer C.M.;
 RT "Complete genome sequence and comparative genomic analysis of an
 RT emerging human pathogen, serotype V Streptococcus agalactiae.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
 CC -1- FUNCTION: This protein is essential for replication of the
 CC chromosome. It is also involved in DNA recombination and repair
 CC (by similarity).
 CC -1- SIMILARITY: Contains 1 SSB domain.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AE014200; AAM99087.1; -
 DR HSSP; P02339; 1EYG.
 DR TIGR; SAG0180;
 DR InterPro; IPR008994; Nucleic_acid_OB.
 DR InterPro; IPR00424; SSB_protein.
 DR InterPro; IPR010913; SS_binding.
 DR Pfam; PF00436; SSB; 1.
 DR TIGRFAMs; TIGR00621; ssb; 1.
 DR PROSITE; PS50935; SSB; 1.
 DR Complete proteome; DNA repair; DNA replication; DNA-binding.
 FT DOMAIN 1 103 SSB.
 SQ SEQUENCE 131 AA; 14775 MW; 5204E89D421B0EDD CRC64;

Query Match 1.3%; Score 7; DB 1; Length 131;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 ETLASYG 67
 Db 59 ETLASYG 65

RESULT 53
 ID Q8ZE27 PRELIMINARY; PRT; 140 AA.
 AC Q8ZE27; Q74U89;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2004 (TREMBlrel. 28, Last sequence update)
 DT 01-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Putative decarboxylase (EC 4.1.1.44).
 GN OrderedLocustNames=YF1846, YP01999;
 OS Yersinia pestis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 NCBI_TaxID=632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=91001 / Biovar Mediaevalis;
 RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
 RA Parkhill J., Wren B.W., Thomson N.R., Tiplall R.M., Holden M.T.G.,
 RA Prentice M.B., Sebahia M., James K.D., Churcher C.M., Mungall K.L.,
 RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.W.,
 RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
 RA Pelletier T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
 RA Leather S., Mouton S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
 RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrett B.G.,
 RA "genome sequence of Yersinia pestis, the causative agent of plague.",
 RT Nature 413:523-527(2001).
 RL [2]
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=91001 / Biovar Mediaevalis;
 RA Song Y., Tong Z., Wang L., Han Y., Zhang J., Pei D., Wang J., Zhou D.,
 RA Han Y., Pang X., Zhai J., Chen F., Qin H., Wang J., Li S., Guo Z.,
 RA Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P.,
 RA Yang R.;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ014151; CAC90812.1; -
 DR EMBL; AE017134; AAS62066.1; -
 DR PIR; AH0243; AH0243.
 DR GO; GO:0047575; F:4-carboxymuconolactone decarboxylase activity; IEA.
 DR GO; GO:0016829; F:lyase activity; IEA.
 DR GO; GO:0006725; P:anabolic compound metabolism; IEA.
 DR InterPro; IPR003779; CMD.
 DR Pfam; PF02627; CMD; 1.
 KM Complete proteome; Lyase.
 SQ SEQUENCE 140 AA; 15578 MW; 6519E30B5B7DC060 CRC64;
 Query Match 1.3%; Score 7; DB 2; Length 140;
 Best Local Similarity 100.0%; Pred.No.2.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RA Yang R.;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE017134; AAS62066.1; -
 SQ SEQUENCE 140 AA; 15578 MW; 6519E30B5B7DC060 CRC64;
 Query Match 1.3%; Score 7; DB 2; Length 140;
 Best Local Similarity 100.0%; Pred.No.2.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 LRSHRL 32
 DB 92 LRSHRL 98

RESULT 54
 ID AAS62066 PRELIMINARY; PRT; 140 AA.
 AC AAS62066;
 DT 24-MAR-2004 (TREMBlrel. 27, Created)
 DT 24-MAR-2004 (TREMBlrel. 27, Last sequence update)
 DT 04-MAY-2004 (TREMBlrel. 27, Last annotation update)
 DE Putative decarboxylase.
 GN YF1846.
 OS Yersinia pestis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 NCBI_TaxID=632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=91001 / Biovar Mediaevalis;
 RA Song Y., Tong Z., Wang L., Han Y., Zhang J., Pei D., Wang J., Zhou D.,
 RA Han Y., Pang X., Zhai J., Chen F., Qin H., Wang J., Li S., Guo Z.,
 RA Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P.,
 RA Yang R.;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ014151; CAC90812.1; -
 DR EMBL; AE017134; AAS62066.1; -
 DR PIR; AH0243; AH0243.
 DR GO; GO:0047575; F:4-carboxymuconolactone decarboxylase activity; IEA.
 DR GO; GO:0016829; F:lyase activity; IEA.
 DR GO; GO:0006725; P:anabolic compound metabolism; IEA.
 DR InterPro; IPR003779; CMD.
 DR Pfam; PF02627; CMD; 1.
 KM Complete proteome; Lyase.
 SQ SEQUENCE 140 AA; 15578 MW; 6519E30B5B7DC060 CRC64;
 Query Match 1.3%; Score 7; DB 2; Length 140;
 Best Local Similarity 100.0%; Pred.No.2.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 LRSHRL 32
 DB 92 LRSHRL 98

RESULT 55
 ID Q973V4 PRELIMINARY; PRT; 141 AA.
 AC Q973V4;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Hypothetical protein ST0794.
 GN OrderedLocustNames=ST0794;
 OS Sulfolobus tokodaii.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 NCBI_TaxID=111955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JCM 10545 / 7;
 RX MEDLINE=21456156; PubMed=11572479;
 RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
 RA Sekine M., Baba S.-I., Ankel A., Kosugi H., Haseyama A., Fukui S.,
 RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
 RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
 RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
 RA Oshima T., Kikuchi H.;
 RL "Complete genome sequence of an aerobic thermophilic
 RT Crenarchaeon, Sulfolobus tokodaii strain7.";
 RL DNA Res. 8:123-140(2001).
 DR EMBL; AP000983; BAB55806.1; -
 DR HSSP; Q9W282; 103U.
 DR InterPro; IPR007842; HEPN.
 DR Pfam; PF05169; HEPN; 1.
 DR SMART; SM00748; HEPN; 1.
 DR PROSITE; PS50910; HEPN; 1.
 KM Complete proteome; Hypothetical protein.
 SQ SEQUENCE 141 AA; 16604 MW; 524D8D3EB9A8F1BF CRC64;
 Query Match 1.3%; Score 7; DB 2; Length 141;
 Best Local Similarity 100.0%; Pred.No.2.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 RVRLLKR 10
 DB 5 RVRLLKR 11

RESULT 56
 ID Q8C938 PRELIMINARY; PRT; 141 AA.
 AC Q8C938;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length
 DE enriched library, clone:AV30050C11 product:hypothetical protein, full
 DE insert sequence (Mouse).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]


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DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE Similar to Drosophila melanogaster CGL696 (Fragment).
OS Drosophila yakuba (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7245;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887302; PubMed=14525923;
RA Domazet-Lošo T., Tautz D.;
RT "An evolutionary analysis of orphan genes in Drosophila.";
RL Genome Res. 13:2213-2219(2003).
DR EMBL; AY231886; AAR09909.1; -.
FT NON_TER 1
FT SEQUENCE 144 AA; 16871 MW; BE0790DFAEBDE3E CRC64;
SQ
Query Match 1.3%; Score 7; DB 2; Length 144;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 348 DVSUVS 354
DB 129 DVSUVS 135

RESULT 60
Q8GDK1 PRELIMINARY; PRT; 148 AA.
ID Q8GDK1;
AC Q8GDK1;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE orf20.
GN Name=orf20;
OS Photorhabdus luminescens (Xenorhabdus luminescens).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
NCBI_TaxID=29488;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22454990; PubMed=12564993;
RA Waterfield N.R., Daborn P.J., French-Constant R.H.;
RT "Genomic islands in Photorhabdus.";
RL Trends Microbiol. 10:541-545(2002).
DR EMBL; AY144118; AAN64224.1; -.
DR InterPro; IPR009063; Bac_Ig/alb_bind.
DR InterPro; IPR007048; GPM_gp25.
DR Pfam; PF04965; GPM_gp25; 1.
SQ SEQUENCE 148 AA; 16800 MW; 8C3B338A167BC3B3 CRC64;
QY 150 SIQDNH 156
DB 21 SIQDNH 27

Query Match 1.3%; Score 7; DB 2; Length 148;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 150 SIQDNH 156
DB 21 SIQDNH 27

RESULT 61
Q94I73 PRELIMINARY; PRT; 149 AA.
ID Q94I73;
AC Q94I73;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical protein OSUJBA0010P20.21.
DE Name=OSUJBA0010P20.21;

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OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RX Huang E.N., de la Bastide M., Vil D.M., Preston R.R., Spiegel L.A.,
RX See L.H., Shah R., Matero A., O'Shaughnessy A., Rodriguez M.,
RX Shekher M., Swaby I., Schutz K., Habermann K., Parnell L.D.,
RA Nascimben L.U., Dedhia N.N., McCombie W.R.;
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC011806; AAK53844.1; -.
DR Gramene; Q94I73; -.
KW Hypothetical protein.
SQ SEQUENCE 149 AA; 15279 MW; 6E8B7E6B53DFF64 CRC64;
QY 504 RPPFRPS 510
DB 86 RPPFRPS 92

Query Match 1.3%; Score 7; DB 2; Length 149;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 504 RPPFRPS 510
DB 86 RPPFRPS 92

RESULT 62
YA87_MYCN STANDARD; PRT; 150 AA.
ID YA87_MYCN
AC P75606;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypothetical protein MPN087 (R02_orf150).
GN OrderedLocustNames=MPN087; ORFNames=MP066;
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2104;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 29342 / M129;
RX MEDLINE=97105885; PubMed=8948633;
RA Himmelfeich R., Hilbert H., Pliagens H., Pirkl E., Li B.-C.,
RA Herrmann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae.";
RL Nucleic Acids Res. 24:4420-4449(1996).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: TO THE CENTRAL SECTION OF M.PNEUMONIAE MPN085.
CC -----
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CC -----
DR EMBL; AE000009; AAB95716.1; -.
DR PIR; S73394; S73394.
KW Complete proteome; Hypothetical protein; Transmembrane.
FT TRANSMEM 48
FT TRANSMEM 68
FT TRANSMEM 89
FT TRANSMEM 109
FT TRANSMEM 123
FT TRANSMEM 143
FT TRANSMEM Potential.
SQ SEQUENCE 150 AA; 17549 MW; FF60FF60C08803B2 CRC64;
QY 328 DVFGLVV 334
DB 94 DVFGLVV 100

Query Match 1.3%; Score 7; DB 1; Length 150;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 328 DVFGLVV 334
DB 94 DVFGLVV 100

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RESULT 63
Q93VE4 PRELIMINARY; PRT; 151 AA.
ID Q93VE4;
AC Q93VE4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE P056B06.34 Protein (P0043B10.26 protein).
GN Name=P056B06.34; Synonyms=P0043B10.26;
OS Oryza sativa (japonica cultivar-group);
OC Eukaryota; Viridiplantae; Streptophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OC NCBI_TaxID=39947;
CX RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsunoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Nishimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hijioka S., Honda M., Ichikawa Y., Ikonuma A., Iijima M., Ikeda M.,
RA Ikono M., Itoh S., Itoh T., Itoh Y., Iwabuchi A., Kamiya K.,
RA Karsawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA Machita K., Maehara T., Mizuno H., Mizutani Y., Nakai Y.,
RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
RA Yano M., Jiang J., Gojobori T.;
RT "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
DR EMBL; AP003281; BAB64766.1; -
DR EMBL; AP003281; BAB64766.1; -
DR Gramene; Q93VE4; -
SQ SEQUENCE 151 AA; 15482 MW; C7FE32E388A4657 CEC64;

Query Match
Best Local Similarity 1.3%; Score 7; DB 2; Length 151;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 504 RPPRPS 510
Db 88 RPPRPS 94

RESULT 64
Q7X9T7 PRELIMINARY; PRT; 152 AA.
ID Q7X9T7;
AC Q7X9T7;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Gbss1-1 protein (Fragment).
GN Name=gbss1-1;
OS Geum rivale;
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Rosales; Rosaceae; Rosoideae; Geum.
OC NCBI_TaxID=148897;
CX RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=22660791; PubMed=12775526;
RA Smedmark U.E., Eriksson T., Evans R.C., Campbell C.S.;
RA "Ancient allopolyploid speciation in Geinae (Rosaceae): evidence from
RA nuclear granule-bound starch synthase (GBSSI) gene sequences.";
RL Syst. Biol. 52:374-385(2003).
DR EMBL; AF534201; CAD59468.1; -
FT NON TER 152 1
FT SEQUENCE 152 AA; 17276 MW; 1B8E4AAC9B005FB CRC64;

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Query Match
Best Local Similarity 1.3%; Score 7; DB 2; Length 152;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 LRLSLIC 36
Db 90 LRLSLIC 96

RESULT 65
P9AA ANACY STANDARD; PRT; 160 AA.
ID P9AA ANACY
AC P07325;
DT 01-APR-1998 (Rel. 07, Created)
DT 01-APR-1998 (Rel. 07, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Allophycocyanin alpha chain.
GN Name=apca;
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OC NCBI_TaxID=1165;
CX RN [1]
RP SEQUENCE.
RA Minami Y., Yamada F., Hase T., Matsubara H., Murakami A., Fujita Y.,
RA Takeo T., Shimonishi Y.;
RT "Amino acid sequences of allophycocyanin alpha- and beta-subunits
RT isolated from Anabaena cylindrica."
RL FEBS Lett. 191:216-220(1985).
CC -1- FUNCTION: Light-harvesting photosynthetic bile pigment-protein
CC from the phycobiliprotein complex. Allophycocyanin has a maximum
CC absorption at approximately 650 nanometers.
CC -1- SUBUNIT: Heterodimer of an alpha and a beta chain.
CC -1- PTM: Contains one covalently linked bilin chromophore.
CC -1- SIMILARITY: Belongs to the phycobiliprotein family.
DR PIR; A24224; AFA1AC.
DR HSSP; P00315; 1B33.
DR InterPro; IPR009050; Globin like.
DR InterPro; IPR001659; Phycobilisome.
DR Pfam; PF00502; Phycobilisome; 1.
DR Pfam; PF000340; Phycobilisome; 1.
KW Bile pigment; Direct protein sequencing; Electron transport;
KW Photosynthesis; Phycobilisome.
FT BINDING 80 80 Phycocyanobilin chromophore.
FT SEQUENCE 160 AA; 17081 MW; 537C408172597624 CRC64;

Query Match
Best Local Similarity 1.3%; Score 7; DB 1; Length 160;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 YGIISGD 72
Db 93 YGIISGD 99

RESULT 66
P9AA_FREDI STANDARD; PRT; 160 AA.
ID P9AA_FREDI
AC P16570;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Allophycocyanin alpha chain 1.
GN Name=apca;
OC Fremyella diplosiphon (Calothrix PCC 7601).
OC Bacteria; Cyanobacteria; Nostocales; Microchaetaceae; Fremyella.
OC NCBI_TaxID=1197;
CX RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=89053869; PubMed=2461358;
RA Hounard V., Courain V., Tandeau de Marsac N.;
RA "Genes encoding core components of the phycobilisome in the
RA cyanobacterium Calothrix sp. strain PCC 7601: occurrence of a

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RT multigene family."
RL J. Bacteriol. 170:5512-5521(1988).
CC -1- FUNCTION: Light-harvesting photosynthetic bile pigment-protein
CC from the phycobiliprotein complex. Allophycocyanin has a maximum
CC absorption at approximately 650 nanometers.
CC -1- SUBUNIT: Heterodimer of an alpha and a beta chain.
CC -1- PTM: Contains one covalently linked bilin chromophore.
CC -1- SIMILARITY: Belongs to the phycobiliprotein family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M20806; AAA24874.1; -.
DR HGSP: P00315; 1B33.
DR InterPro: IPR009050; Globin-like.
DR InterPro: IPR001659; Phycobillism.
DR Pfam: PF00502; Phycobillism; 1.
DR ProDom: PD000340; Phycobillism; 1.
KM Bile pigment; Electron transport; Photosynthesis; Phycobillism.
FT INIT MET 0
FT BINDING 80 80 Phycocyanobilin chromophore.
SQ SEQUENCE 160 AA; 17233 MW; 9C6E55F6A4923C29 CRC64;

Query Match 1.3%; Score 7; DB 1; Length 160;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 YGIVSGD 72
DB 93 YGIVSGD 99

RESULT 67
PHAA_PORYE STANDARD; PRT; 160 AA.
ID PHAA_PORYE
AC P59856;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Allophycocyanin alpha chain.
GN Name=apca;
OS Porphyra yezoensis.
OG Chloroplast.
OC Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.
OX NCBI_TaxID=2788;
RN [1]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=99287890; Pubmed=10358042;
RA Liu J.Y., Jiang T., Zhang J.P., Liang D.C.;
RT "Crystal structure of allophycocyanin from red algae Porphyra
RT yezoensis at 2.2-A resolution."
RL J. Biol. Chem. 274:16945-16952(1999).
CC -1- FUNCTION: Light-harvesting photosynthetic bile pigment-protein
CC from the phycobiliprotein complex. Allophycocyanin has a maximum
CC absorption at approximately 650 nanometers.
CC -1- SUBUNIT: Heterodimer of an alpha and a beta chain.
CC -1- PTM: Contains one covalently linked bilin chromophore.
CC -1- SIMILARITY: Belongs to the phycobiliprotein family.
CC -----
DR InterPro: IPR001659; Phycobillism.
DR Pfam: PF00502; Phycobillism; 1.
DR ProDom: PD000340; Phycobillism; 1.
KM 3D-structure; Bile pigment; Chloroplast; Electron transport;
KW Photosynthesis; Phycobillism.
FT INIT MET 0
FT BINDING 80 80 Phycocyanobilin chromophore.
SQ SEQUENCE 160 AA; 17366 MW; 4CCCB87BD67B23D CRC64;

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Query Match 1.3%; Score 7; DB 1; Length 160;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 YGIVSGD 72
DB 93 YGIVSGD 99

RESULT 68
Q8DU53 PRELIMINARY; PRT; 160 AA.
ID Q8DU53;
AC Q8DU53;
DT 01-MAR-2003 (TRMBLrel. 23, Created)
DT 01-MAR-2003 (TRMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TRMBLrel. 26, Last annotation update)
DE Putative transcriptional regulator protein.
GN Ordered locus names=SMO.1097c;
OS Streptococcus mutans.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1309;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UAI59 / ATCC 700610 / Serotype C;
RX MEDLINE=22295063; Pubmed=12397186; DOI=10.1073/pnas.172501299;
RA Ajdic D.J., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
RA Carson M.B., Primeaux C., Tian R., Kenton S., Jia H.G., Lin S.P.,
RA Qian Y., Li S., Zhu H., Najjar F.Z., Lai H., White J., Roe B.A.,
RA Ferretti J.J.;
RT "Genome sequence of Streptococcus mutans UAI59, a cariogenic dental
RT pathogen."
RL Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).
CC -1- SIMILARITY: Contains 1 HTH matr-type DNA-binding domain.
DR EMBL: AB014947; AAN58794.1; -.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000835; HTH_Matr.
DR InterPro: IPR009058; wing_hlx_DNA_bnd.
DR Pfam: PF01047; Mair; 1.
DR SMART: SM00347; HTH_MARR; 1.
SQ Complete proteome: DNA-binding; Transcription regulation.
SQ SEQUENCE 160 AA; 18693 MW; 094B79A612C122A CRC64;

Query Match 1.3%; Score 7; DB 2; Length 160;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 260 VYNATLK 266
DB 64 VYNATLK 70

RESULT 69
Q96NMO PRELIMINARY; PRT; 163 AA.
ID Q96NMO;
AC Q96NMO;
DT 01-DEC-2001 (TRMBLrel. 19, Created)
DT 01-DEC-2001 (TRMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TRMBLrel. 22, Last annotation update)
DE Hypothetical protein FLJ32172.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Placenta;
RX Pubmed=14702039;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Oobayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

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RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahashi K.,
 RA Murakami K., Yasuda T., Iwayanagi T., Nagatsuna M., Shiratori A.,
 RA Sudo H., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
 RA Nishimura K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
 RA Tani H., Kimura M., Watanabe M., Hiyosaka S., Chiba Y., Ishida S.,
 RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Horita T., Kusano J.,
 RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nemura Y.,
 RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
 RA Mitsuhashi K., Yuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Kawakami B.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Taketono M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujitani T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hiroo M., Ohno Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Ohtani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senda T.,
 RA Matsunura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togaishi T., Oyama M., Hara H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shitai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
 RT "Complete sequencing and characterization of 21,243 full-length human
 cDNAs.";
 RL Nat. Genet. 36:40-45(2004).
 DR EMBL, AK056734, BAB1267.1, -
 SQ SEQUENCE 163 AA; 18797 MW; B69B19F5FC0E1A07 CRC64;

Query Match 1.3%; Score 7; DB 2; Length 163;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 321 RQALNLP 327
 Db 4 RQALNLP 10

RESULT 70
 Q70IG5 PRELIMINARY; PRT; 166 AA.
 AC Q70IG5;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 GN AGCP3440 (Fragment).
 GN Name=agcG54193; ORFNames=ENSANG00000010761;
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoides; Anopheles.
 OC NCBI_TaxID=180454;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PEST;
 RA Anopheles Genome Sequencing Consortium;
 RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 CC EMBL: AAA501008807; EAA04291.1;
 DR GO: GO:0042302; F: structural constituent of cuticle; IEA.
 DR InterPro: IPR000618; Insect_cuticle.
 DR Pfam: PF00379; Cuticn_bind_4; 1.
 DR PRINTS: PR00947; CUTICLE.
 DR PROSITE: PS00233; CUTICLE; UNKNOWN_1.
 RT NON TER
 FT 1
 SQ SEQUENCE 166 AA; 18911 MW; 95B3773EDD2F781D CRC64;

Query Match 1.3%; Score 7; DB 2; Length 166;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 KDPLTGD 59
 Db 78 KDPLTGD 84

RESULT 71
 Q8G4L5 PRELIMINARY; PRT; 166 AA.
 AC Q8G4L5;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 GN Ordered locus names=B13164;
 OS Bifidobacterium longum.
 OC Bacteria; Actinobacteriae; Bifidobacteriales;
 OC Bifidobacteriaceae; Bifidobacterium.
 OC NCBI_TaxID=216816;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCC 2705;
 RX MEDLINE=22294977; PubMed=12381787;
 RA Schell M.A., Kamitzantzu M., Snel B., Vilanova D., Berger B.,
 RA Pessi G., Zwielen W.-C., Desiere F., Bork P., Delley M.,
 RA Pridmore R.D., Arigoni F.,
 RT "The genome sequence of Bifidobacterium longum reflects its adaptation
 to the human gastrointestinal tract.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
 RL EMBL, AE014766; AAN25164.1; -
 DR Complete proteome; Hypothetical protein.
 KW SEQUENCE 166 AA; 17619 MW; 863A301DD8DBAE2D CRC64;

Query Match 1.3%; Score 7; DB 2; Length 166;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 515 TDGRLSF 521
 Db 59 TDGRLSF 65

RESULT 72
 Q97H82 PRELIMINARY; PRT; 167 AA.
 AC Q97H82;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein CAC2131.
 GN Ordered locus names=CAC2131;
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OC NCBI_TaxID=1488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE=21359325; PubMed=11466286;
 RX DOI=10.1128/JB.185.16.4623-4638.2001;
 RA Noelling U., Breton G., Ometchenko M.V., Makarova K.S., Zeng Q.,
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hilti U., Wolf Y.I.,
 RA Tatunov R.L., Sabatche F., Doucette-Stamm L.A., Soucaille P.,
 RA Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.,
 RT "Genome sequence and comparative analysis of the solvent-producing
 bacterium Clostridium acetobutylicum.";
 RL J. Bacteriol. 183:4823-4838(2001).
 DR EMBL, AE007714; AAK80089.1; -
 DR PIR; F97162; F97162.
 KM Complete proteome; Hypothetical protein.
 SQ SEQUENCE 167 AA; 19373 MW; 386752F8386ED78 CRC64;

Query Match 1.3%; Score 7; DB 2; Length 167;

Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 339 LKTRIR 345
Db 103 LKTRIR 109

RESULT 73

QY 07V177 PRELIMINARY; PRT; 170 AA.
ID 07V177;
AC 07V177;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Glutathione peroxidase [EC 1.11.1.9].
GN OrderedAccession=PM1006;
OS Prochlorococcus marinus subsp. pastoris (strain CCMP 1378 / MED4).
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcales;
OC Prochlorococcus.
OC NCBI_TaxID=59919;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2825686; PubMed=12917642; DOI=10.1038/nature01947;
RA Roca G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P.,
RA Algren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
RA Johnson Z.I., Arellano A., Lindell D., Post A.F., Regala W., Shah M.,
RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
RA Webb E.A., Zinner E.R., Chisholm S.W.;
RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
niche differentiation."
RT Nature 424:1042-1047(2003).
RL -1- SIMILARITY: Belongs to the glutathione peroxidase family.
CC EMBL; BX572092; CAB19465.1; -
DR GO: GO:0004602; F:Glutathione peroxidase activity; IEA.
DR GO: GO:0016491; F:oxidoreductase activity; IEA.
DR GO: GO:0004601; F:peroxidase activity; IEA.
DR GO: GO:0006979; F:response to oxidative stress; IEA.
DR InterPro; IPR000889; Glut_Peroxidase.
DR Pfam; PF00255; GSHpx; 1.
DR PROSITE; PS00460; GLUTATHIONE PEROXID 1; 1.
KM Complete proteome; Oxidoreductase; Peroxidase.
SQ SEQUENCE 170 AA; 18947 MW; 83189938CED621F CRC64;

Query Match 1.3%; Score 7; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 298 YKDLQKL 304
Db 54 YKDLQKL 60

RESULT 74

QY 08T018 PRELIMINARY; PRT; 172 AA.
ID 08T018
AC 08T018;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE GH27769P.
GN ORFNames=CG9619;
OS Drosophila melanogaster (Fruit Fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Eurytomidae; Drosophilidae; Drosophila.
OC NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RA Chapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise B., George R.,
RA Gonzalez W., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.;

RA Nunoo J., Paclieb J., Paragas V., Park S., Phuanenavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celinker S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY069230; AL39375.1; -
DR FlyBase; FBgn0036862; CG9619.
DR InterPro; IPR005036; CEM_21.
DR Pfam; PF03370; CEM_21; 1.
SQ SEQUENCE 172 AA; 18713 MW; FE0D1923C2A3F6F3 CRC64;

Query Match 1.3%; Score 7; DB 2; Length 172;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 415 LPSTHT 421
Db 125 LPSTHT 131

RESULT 75

QY 07XJ34 PRELIMINARY; PRT; 182 AA.
ID 07XJ34
AC 07XJ34;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Dechlorated1 (Fragment).
OS Brassica rapa subsp. pekinensis (Chinese cabbage) (Celery cabbage).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Eusterois II; Brassicales; Brassicaceae; Brassica.
OC NCBI_TaxID=51351;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RA Tang H.S., Hur Y.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY34835; AAP92379.1; -
FT NON_TER 182
FT NON_TER 182
SQ SEQUENCE 182 AA; 21273 MW; 2C47973EB9C7F5BC CRC64;

Query Match 1.3%; Score 7; DB 2; Length 182;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 382 DNTVRVQ 388
Db 150 DNTVRVQ 156

Search completed: November 16, 2004, 07:30:56
Job time : 202 secs

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OM protein - protein search, using sw model

Run on: November 16, 2004, 07:13:20 ; Search time 155 Seconds
(without alignments)
1208.108 Million cell updates/sec

Title: US-09-927-458-2

Perfect score: 522
Sequence: 1 MLRLVRLKRWLPLEVPETE.....DRFPFRPSRGHPTDRLSFM 522

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2002273 seqs, 358729299 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : A_Geneseq_23Sep04:*

1: geneseqp1980s:*\n2: geneseqp1990s:*\n3: geneseqp2000s:*\n4: geneseqp2001s:*\n5: geneseqp2002s:*\n6: geneseqp2003as:*\n7: geneseqp2003bs:*\n8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	490	93.9	522	6	ADAs7283 Human sec
2	490	93.9	522	6	ADAA1163
3	490	93.9	522	6	ABR47958 Human sec
4	490	93.9	522	7	ADCT74366 Human sec
5	417	79.9	591	2	AAW68521 Human RIP
6	389	74.5	522	4	AAAB35161 Human Sxp
7	354	67.8	607	4	AAU32109 Novel hum
8	330	63.2	443	4	AAAB35160 Human hum
9	271	51.9	317	7	ABBB90108 Human pol
10	231	44.3	231	7	ADJ68946 Human hea
11	231	44.3	221	6	ADAs4155 Human pro
12	200	38.3	462	5	ABBB90109 Human pol
13	200	38.3	462	6	ADAs7586 Human sec
14	200	38.3	462	6	ADAA1482 Human sec
15	200	38.3	462	6	ABR48139 Human sec
16	200	38.3	462	6	ADCT4596 Human sec
17	200	38.3	462	4	ABG18510 Novel hum
18	134	25.7	549	4	ADAs7587 Human sec
19	128	24.5	174	6	ADAA1483 Human sec
20	128	24.5	174	6	ABR48140 Human sec
21	128	24.5	174	6	ADCT4597 Human sec
22	128	24.5	175	7	AAAY41397 Human sec
23	86	16.5	482	3	AAV83047 F-box pro
24	86	16.5	482	3	AAO22452 Human F-b
25	76	14.6	76	8	ABO54274 Human gen

26	63	12.1	94	4	AAU32107	AAU32107 Novel hum
27	59	11.3	113	3	AAAY87356	AAAY87356 Human sig
28	53	10.2	225	4	ABG06838	ABG06838 Novel hum
29	47	9.0	47	8	ABO59862	ABO59862 Human gen
30	39	7.5	39	3	AAAY83054	AAAY83054 F-box mot
31	39	7.5	39	3	AAO22455	AAO22455 Human F-b
32	38	7.3	38	2	AAAY02272	AAAY02272 A F-box p
33	38	7.3	38	4	AAE08044	AAE08044 Human F-b
34	38	7.3	38	7	AAE39652	AAE39652 Human F-b
35	32	6.1	53	4	ABG18509	ABG18509 Novel hum
36	32	6.1	53	4	AAU32108	AAU32108 Novel hum
37	32	2.9	38	2	AAAY02272	AAAY02272 A F-box p
38	38	2.9	38	4	AAE08045	AAE08045 Human F-b
39	15	2.9	38	7	AAE39653	AAE39653 Mouse F-b
40	13	2.5	13	2	AAAY41578	AAAY41578 Fragment
41	13	2.5	13	2	AAAY41577	AAAY41577 Fragment
42	8	1.5	57	4	AAAG94240	AAAG94240 Human rep
43	8	1.5	63	8	ABO55854	ABO55854 Human gen
44	8	1.5	92	5	ABP10900	ABP10900 Human ORF
45	8	1.5	183	6	AAU55117	AAU55117 Proponib
46	8	1.5	183	6	ABM51636	ABM51636 Proponib
47	8	1.5	572	3	AAAG32036	AAAG32036 Arabidops
48	8	1.5	628	4	AAAG66450	AAAG66450 Murine be
49	8	1.5	789	6	ABU21326	ABU21326 Protein e
50	5	1.3	13	7	ADCS4146	ADCS4146 Peptide 1
51	5	1.3	20	2	AAAY72285	AAAY72285 Glutamic
52	5	1.3	20	3	AAAY59556	AAAY59556 GAD65 fra
53	5	1.3	26	7	ADCS4148	ADCS4148 Peptide 1
54	5	1.3	32	7	ADM08067	ADM08067 Canine im
55	5	1.3	32	7	ADM08066	ADM08066 Canine im
56	5	1.3	32	7	ADM07905	ADM07905 Canine im
57	5	1.3	32	7	ADM08430	ADM08430 Canine im
58	5	1.3	32	7	ADM08148	ADM08148 Canine im
59	5	1.3	32	7	ADM07907	ADM07907 Canine im
60	5	1.3	32	7	ADM07904	ADM07904 Canine im
61	5	1.3	32	7	ADM08347	ADM08347 Canine im
62	5	1.3	32	7	ADM08348	ADM08348 Canine im
63	5	1.3	32	7	ADM08442	ADM08442 Canine im
64	5	1.3	32	7	ADM07910	ADM07910 Canine im
65	5	1.3	32	7	ADM08438	ADM08438 Canine im
66	5	1.3	32	7	ADM08062	ADM08062 Canine im
67	5	1.3	32	7	ADM08336	ADM08336 Canine im
68	5	1.3	58	6	ADAs7203	ADAs7203 Human sec
69	5	1.3	58	6	ADAA1080	ADAA1080 Human sec
70	5	1.3	58	6	ABR47918	ABR47918 Human sec
71	5	1.3	59	2	AAAY36325	AAAY36325 Human sec
72	5	1.3	59	3	AAAY73500	AAAY73500 Human sec
73	5	1.3	59	6	ADAA11698	ADAA11698 Human nov
74	5	1.3	63	6	ABBS5962	ABBS5962 Manduca s
75	5	1.3	64	6	ABBS5961	ABBS5961 Manduca s
76	5	1.3	64	6	AAU42520	AAU42520 Proponib
77	5	1.3	64	6	ABM39039	ABM39039 Proponib
78	5	1.3	65	4	AAU18916	AAU18916 Novel pro
79	5	1.3	65	4	AAAY68229	AAAY68229 Human rep
80	5	1.3	66	4	ABM47355	ABM47355 Proponib
81	5	1.3	66	6	ABM47356	ABM47356 Proponib
82	5	1.3	76	6	ABM36050	ABM36050 Proponib
83	5	1.3	83	3	AAAG03130	AAAG03130 Human sec
84	5	1.3	89	4	AAU18904	AAU18904 Peptide #
85	5	1.3	89	4	ABR38029	ABR38029 Peptide #
86	5	1.3	89	4	AAAY31445	AAAY31445 Peptide #
87	5	1.3	89	4	ABB23262	ABB23262 Protein #
88	5	1.3	89	4	AAW71164	AAW71164 Human don
89	5	1.3	89	4	AAW58658	AAW58658 Human bra
90	5	1.3	89	5	ABG52876	ABG52876 Human liv
91	5	1.3	89	5	ABG40961	ABG40961 Human pep
92	5	1.3	90	8	ABO60647	ABO60647 Human gen
93	5	1.3	92	4	ABBI5782	ABBI5782 Human ner
94	5	1.3	93	4	AAU17900	AAU17900 Novel hum
95	5	1.3	93	6	ABU44049	ABU44049 Protein e
96	5	1.3	93	7	ADGA1280	ADGA1280 Human tes
97	5	1.3	101	4	AAW95027	AAW95027 Human rep
98	7	1.3				

ALIGNMENTS

99 7 1.3 104 5 ADK34930 Novel hum
100 7 1.3 107 4 AAU45802 Aau45802 Propionib

RESULT 1
ID ADAS7283 standard; protein; 522 AA.

ADAS7283;
AC ADAS7283;
XX 20-NOV-2003 (first entry)
XX
XX Human secreted protein #566.
DE
XX immunosuppressive; antiinflammatory; antiasthmatic; anti-allergic;
KW cytostatic; cerebroprotective; neuroprotective; neurotropic;
KW cardiovascular; antiarteriosclerotic; gene therapy;
KW human secreted protein; immune disorder; inflammation;
KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;
KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;
KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;
KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;
KW triple helix formation; antisense gene therapy; forensic biology.

XX Homo sapiens.
OS
XX WO2002102994-A2.
XX
XX 27-DEC-2002.
XX
XX 19-MAR-2002; 2002WO-US008278.
XX
XX 21-MAR-2001; 2001US-0277340P.
XX 19-JUL-2001; 2001US-0306171P.
XX 13-NOV-2001; 2001US-0331287P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM;
XX WPI; 2003-167512/16.
XX N-PSDB; ADA56387.
XX
XX New human secreted polypeptides and polynucleotides, useful for
XX diagnosing, treating or preventing e.g. immune disorders, inflammatory
XX conditions, respiratory disorders, cancers, CNS disorders, or
XX neurodegenerative disorders, or polypeptides comprising an amino acid
XX sequence at least 95% identical to the new sequences. The polypeptides,
XX antibodies or antibody fragments that bind to the polypeptides, nucleic
XX acids encoding the polypeptides, agonists or antagonists that binds to
XX the polypeptide, are useful in preparing diagnostic or pharmaceutical
XX compositions for diagnosing, treating or preventing an e.g. immune
XX disorders, inflammatory conditions (e.g. inflammatory bowel disease,
XX nephritis or Crohn's disease), respiratory disorders (e.g. asthma and
XX allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
XX (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative
XX disorders (e.g. Parkinson's disease or Alzheimer's disease), and
XX cardiovascular disorders (e.g. atherosclerosis or myocarditis). The
XX polynucleotides are useful for chromosome identification, chromosome
XX mapping, for controlling gene expression through triple helix formation
XX or antisense DNA or RNA, in gene therapy, for identifying individuals
XX from minute biological samples, in forensic biology, and as hybridization
XX probes. The polypeptides are useful for as molecular weight markers on

CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
CC gels, to raise antibodies, for testing biological activities, and for
CC treating or preventing neural disorders, immune system disorders,
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC renal, proliferative and/or cancerous diseases. This sequence corresponds
CC to one of the polypeptide of the invention. Note: The sequence data for
CC this patent did form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 522 AA;

Query Match 93.9%; Score 490; DB 6; Length 522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 490; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 SLCTMGVSSNRTFTTNTYKDLTGDEETLASVGVSGDLICLLDIDPAPNIPSSD 92
DB 33 SLCTMGVSSNRTFTTNTYKDLTGDEETLASVGVSGDLICLLDIDPAPNIPSSD 92
QY 93 SEHSILQNNNEQPSLATSSNQTSMDQEPSDSFOGQAQSGVWVNDMSMGPSQNFPAESIQ 152
DB 93 SEHSILQNNNEQPSLATSSNQTSMDQEPSDSFOGQAQSGVWVNDMSMGPSQNFPAESIQ 152
QY 153 DNAHAAEGTGFYSPFPMCLSESVESQVPHSLFTLYQSDADCDANDALIVLHLMLESGY 212
DB 153 DNAHAAEGTGFYSPFPMCLSESVESQVPHSLFTLYQSDADCDANDALIVLHLMLESGY 212
QY 213 IPQTEAKALSMPEKMLSGVYKLOYMHPLDESSATTCVPLGNLYVNTATLKINNEIR 272
DB 213 IPQTEAKALSMPEKMLSGVYKLOYMHPLDESSATTCVPLGNLYVNTATLKINNEIR 272
QY 273 SVKRLQLLPESTICEKXGENVANITYKDLQKLSRLFKQOLVYPLAFTROALNPDVFG 332
DB 273 SVKRLQLLPESTICEKXGENVANITYKDLQKLSRLFKQOLVYPLAFTROALNPDVFG 332
QY 333 VVLPELKLRIEFLRLDVAVSLSLSAVCRDLFTASNDPLMRFLYLRDPRDVTVPVOPDW 392
DB 333 VVLPELKLRIEFLRLDVAVSLSLSAVCRDLFTASNDPLMRFLYLRDPRDVTVPVOPDW 392
QY 333 KELYKRKHIOREKESKGFVYLLPESSTHTIPYPNPPLMRPSSRLPPGIIGGEYDQRP 452
DB 333 KELYKRKHIOREKESKGFVYLLPESSTHTIPYPNPPLMRPSSRLPPGIIGGEYDQRP 452
QY 453 TLPIYGDPISSILPEPGTPOFPPLRPPVCPPLPSPNITLGRGPNRPPRPBPG 512
DB 453 TLPIYGDPISSILPEPGTPOFPPLRPPVCPPLPSPNITLGRGPNRPPRPBPG 512
QY 513 RPTDGRLSFM 522
DB 513 RPTDGRLSFM 522

RESULT 2
ADA41163
ID ADA41163 standard; protein; 522 AA.
XX
XX ADA41163;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human secreted protein.
XX
XX Human; secreted protein; cancer; hyperproliferative disorder;
XX rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;
XX anaemia; allergic reaction; asthma; cardiovascular disorder;
XX wound healing; cytostatic; immunosuppressive; neurotropic; neuroprotective;
XX antiviral; anti-allergic; hepatotropic; antidiabetic; anti-inflammatory;
XX vulnerary; candidate; gene therapy.
XX
XX Homo sapiens.
XX
XX WO2002102993-A2.

XX 27-DEC-2002.
 XX
 PF 19-MAR-2002; 2002WO-US008123.
 XX
 PR 21-MAR-2001; 2001US-0277340P.
 PR 19-JUL-2001; 2001US-0306171P.
 PR 13-NOV-2001; 2001US-0331287P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM;
 XX
 DR WPI; 2003-175238/17.
 XX
 PT New human secreted proteins and nucleic acid molecules, useful for
 PT preparing a diagnostic or pharmaceutical composition for diagnosing,
 PT preventing or treating cancer or other hyperproliferative disorder,
 PT asthma, allergies or AIDS.
 PS
 PS Claim 1; SEQ ID NO 1545; 3205bp; English.
 XX
 CC The invention relates to novel genes ADA39629-ADA40565 and proteins
 CC ADA40566-ADA41501 for human secreted proteins, useful for preventing,
 CC treating or ameliorating medical conditions e.g. by protein or gene
 CC therapy. The polypeptides, nucleic acid molecules, antibodies or their
 CC fragments, and agonists or antagonists that bind to the polypeptide are
 CC useful for preparing a diagnostic or pharmaceutical composition for
 CC diagnosing or treating cancer or other hyperproliferative disorder. The
 CC polypeptides and nucleic acid molecules are also useful for detecting,
 CC preventing, diagnosing, prognosticating, treating or ameliorating cancer
 CC or other hyperproliferative disorders including neoplasms, autoimmune
 CC disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus
 CC erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic
 CC anaemia), haematopoietic or haematological disorders (e.g. anaemia,
 CC thrombocytopenia), allergic reactions including asthma or eczema,
 CC inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory
 CC bowel disease or Crohn's disease), neurodegenerative disorders (e.g.
 CC Alzheimer's disease or Parkinson's disease), cardiovascular disorders
 CC (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,
 CC fungal or viral infections including HIV/AIDS), or wound healing and
 CC disorders of epithelial cell proliferation. The nucleic acids are also
 CC useful for chromosome identification, radiation hybrid mapping or long-
 CC range restriction mapping, as molecular weight markers, or as
 CC hybridization or diagnostic probes. The polypeptides and antibodies are
 CC useful for providing immunological probes for differential identification
 CC of the tissues immunohistochemistry assays. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX
 SQ Sequence 522 Aa;

Query Match 93.9%; Score 490; DB 6; Length 522;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 490; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 SLCTGYSNTRFTTLNWKDPLTNGDETLASXGVSGDLICLIQDDIPRNPISSTD 92
 DB 33 SLCTGYSNTRFTTLNWKDPLTNGDETLASXGVSGDLICLIQDDIPRNPISSTD 92
 QY 93 SEHSLSQNNQEPPLATSSNOTSWMODQPSDSFGQAAGVWDDSMGLPSONFEAESIQ 152
 DB 93 SEHSLSQNNQEPPLATSSNOTSWMODQPSDSFGQAAGVWDDSMGLPSONFEAESIQ 152
 QY 153 DNHMAEGRTFYSEPMGLCSSEYSGOVPHSLTLYSACCSDDANALYLHLMLESGY 212
 DB 153 DNHMAEGRTFYSEPMGLCSSEYSGOVPHSLTLYSACCSDDANALYLHLMLESGY 212
 QY 213 IPGTAKALSMPEKKLSGVYVLQVMHPCEGSSATLTCVPLGNLIVNATLKINNEIR 272
 DB 213 IPGTAKALSMPEKKLSGVYVLQVMHPCEGSSATLTCVPLGNLIVNATLKINNEIR 272

QY 273 SVKSLQLLPESFICEKXGENVANITYKLOKLSRLFKDQIVYPLAFTPOALNLPDVGL 332
 DB 273 SVKSLQLLPESFICEKXGENVANITYKLOKLSRLFKDQIVYPLAFTPOALNLPDVGL 332
 QY 333 VLPLELKLRTFRLLDVRYSVLSAVCRDLPFTASNDPLMRFLYLRDPNDTVAVQDTDW 392
 DB 333 VLPLELKLRTFRLLDVRYSVLSAVCRDLPFTASNDPLMRFLYLRDPNDTVAVQDTDW 392
 QY 393 KELYRKHIQKESPKGRFVWLPLPSSTHTTIPVENPLHPPRPPESRPPGGIGGEYQORP 452
 DB 393 KELYRKHIQKESPKGRFVWLPLPSSTHTTIPVENPLHPPRPPESRPPGGIGGEYQORP 452
 QY 453 TLPYGDPISSLLPGPETSQFPPLRPFRDPVGPPLDGPNNILPGRGQPNDRPFPSRG 512
 DB 453 TLPYGDPISSLLPGPETSQFPPLRPFRDPVGPPLDGPNNILPGRGQPNDRPFPSRG 512
 QY 513 RPTDGRUSFM 522
 DB 513 RPTDGRUSFM 522

RESULT 3

ID ABR47958 standard; protein, 522 Aa.

ABR47958;

12-JUN-2003 (first entry)

Human secreted protein, SEQ ID 849.

Cardiac; antiarrhythmic; antiarteriosclerotic; vasotropic; cyostatic;
 vulnerability; antiinflammatory; neurotropic; neuroprotective;
 antiparkinsonian; gene therapy; human; cardiovascular disorder.

Homo sapiens.

WO200295010-A2.

28-NOV-2002.

19-MAR-2002; 2002WO-US009785.

21-MAR-2001; 2001US-0277340P.

19-JUL-2001; 2001US-0306171P.

13-NOV-2001; 2001US-0331287P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Ruben SM;

WPI; 2003-129429/12.

Novel human secreted proteins, useful for detecting, preventing,
 diagnosing, prognosticating, treating and/or ameliorating cardiovascular
 disorders such as arrhythmia.

Claim 13; SEQ ID NO 849; 1881bp; English.

The present invention relates to novel human secreted proteins (ABR47633-
 ABR48145) and their coding sequences (ACC50344-ACC50856). The proteins
 and their coding sequences are useful for the preparation of a diagnostic
 or pharmaceutical composition for diagnosing or treating a cardiovascular
 disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary
 arteriosclerosis and myocardial ischaemia), neural disorders, immune
 system disorders, muscular disorders, reproductive disorders,
 gastrointestinal disorders, pulmonary disorders, renal disorders,
 proliferative disorders and/or cancerous diseases and conditions, for
 wound healing and epithelial cell proliferation, to treat inflammation or
 infection, for treating thrombosis and arteriosclerosis, for treating or
 preventing neural conditions which occurs in neural disorders or
 neurodegenerative conditions such as Alzheimer's disease and Parkinson's
 disease, to enhance bone and periodontal regeneration and aid in tissue

transplants or bone grafts, to prevent skin aging or hair loss, to stimulate growth and differentiation of haematopoietic cells and bone marrow cells when used in combination with other cytokines, to maintain organs before transplantation or for supporting cell culture of primary tissues, to increase or decrease differentiation or proliferation of embryonic stem cells, or to modulate mammalian characteristics or metabolism. Note: The sequence data for this patent was published in electronic format and is available from WIND at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences)

Sequence 522 AA:

Query Match 93.9%; Score 490; DB 6; Length 522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 490; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 33 SLCTWGYSSNTRFTITLNYKDPPLTGDEETLASGIYSGDLICILLODDIPAPNIPSSSTD 92
DB 33 SLCTWGYSSNTRFTITLNYKDPPLTGDEETLASGIYSGDLICILLODDIPAPNIPSSSTD 92
QY 93 SEHSSLQNNNEOPLATSSNOTSMODEQPSDSFOGQAQSGVWVNDMSMLGPSQNFEBASIQ 152
DB 93 SEHSSLQNNNEOPLATSSNOTSMODEQPSDSFOGQAQSGVWVNDMSMLGPSQNFEBASIQ 152
QY 153 DNAMHAGTGTFYPSPEPMUCSBSVSGVPHSLFTLYQSADCSANDALIVLHLMESGY 212
DB 153 DNAMHAGTGTFYPSPEPMUCSBSVSGVPHSLFTLYQSADCSANDALIVLHLMESGY 212
QY 213 IPQTEAKALSMPEKMLSGYKLYQYHPLCEGSSATLTCVPGNLIIVNATLKINNEIR 272
DB 213 IPQTEAKALSMPEKMLSGYKLYQYHPLCEGSSATLTCVPGNLIIVNATLKINNEIR 272
QY 273 SVKRLQLLPESFTCEKLGENVANITYDLOKLSLRFDOJLVPLAFTROALNLPDVFG 332
DB 273 SVKRLQLLPESFTCEKLGENVANITYDLOKLSLRFDOJLVPLAFTROALNLPDVFG 332
QY 333 VVLELELKLRIPLLDVRSVLSAVCRDLFTASNDPLMRFLYRDFRNTVAVQDTDM 392
DB 333 VVLELELKLRIPLLDVRSVLSAVCRDLFTASNDPLMRFLYRDFRNTVAVQDTDM 392
QY 393 KELYKXKHIOKESPKGRFVLLPSSSTHTIPFYNPPLHPPFPSSRLPGIIGEDYDQR 452
DB 393 KELYKXKHIOKESPKGRFVLLPSSSTHTIPFYNPPLHPPFPSSRLPGIIGEDYDQR 452
QY 453 TLPIVGPDISLIGPBTBQFPPLRPFPVGLPGPNLIPGRGQVNDRRPFRPSRG 512
DB 453 TLPIVGPDISLIGPBTBQFPPLRPFPVGLPGPNLIPGRGQVNDRRPFRPSRG 512
QY 513 RPTDGRLSFM 522
DB 513 RPTDGRLSFM 522
Db 513 RPTDGRLSFM 522

RESULT 4
ADCT4366
ID ADCT4366 standard; protein; 522 AA.
XX
AC ADCT4366;
DT 01-JAN-2004 (first entry)
XX
XX Human secreted protein - SEQ ID 999.
DE
XX antianaemic; antirheumatic; antiarthritic; antinflammatory; antithyroid;
KW antidiabetic; immunosuppressive; dermatological; nephrotoxic;
KW antiparkinsonian; neuroprotective; nootropic; antibacterial; vinuclid;
KW fungicide; antiparasitic; antiarteriosclerotic; vulnerary; cytosstatic;
KW haemopoietic; haematologic; anaemia; autoimmune disorder;
KW rheumatoid arthritis; inflammation; Grave's disease; diabetes;
KW systemic lupus erythematosus; glomerulonephritis; neurodegenerative;
KW Parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis;
KW cancer; bacterial; viral; fungal; parasitic infection; gene therapy;
KW human.
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XX OS Homo sapiens.
XX MO2003038063-A2.
XX 08-MAY-2003.
XX 19-MAR-2002; 2002WO-US008277.
XX 21-MAR-2001; 2001US-0277340P.
XX 19-JUL-2001; 2001US-0306171P.
XX 13-NOV-2001; 2001US-0331287P.
XX (HUMA-) HUMAN GENOME SCT INC.
XX Rosen CA, Ruben SM;
XX MPI: 2003-430516/40.
XX N-PSDB; ADCT3751.
XX
XX New human secreted polypeptide for diagnosing, preventing or treating
XX haematopoietic or hematologic disorders (e.g. anemia), autoimmune
XX disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer or
XX atherosclerosis).
XX
XX Claim 16; SEQ ID NO 999; 2272PP; English.
XX
XX The invention relates to a novel human secreted polypeptide comprising a
XX defined sequence given in the specification. The polypeptide, nucleic
XX acid molecule, antibody, agonist or antagonist of the invention may be
XX useful for preparing a composition for diagnosing or treating a
XX haematopoietic or hematologic disorder such as anaemia, autoimmune
XX disorders such as rheumatoid arthritis, inflammation, Grave's disease,
XX diabetes, systemic lupus erythematosus or glomerulonephritis,
XX neurodegenerative disorders including Parkinson's disease and Alzheimer's
XX disease, wounds and hyperproliferative disorders including
XX atherosclerosis or cancer, as well as bacterial, viral, fungal or
XX parasitic infections. The polypeptide may also be used during gene
XX therapy procedures and for identifying a binding partner by contacting
XX the polypeptide with a binding partner and determining whether the
XX binding partner increases or decreases the activity of the polypeptide.
XX The current sequence is that of the human secreted protein of the
XX invention.
XX
XX Sequence 522 AA;
XX
XX Query Match 93.9%; Score 490; DB 7; Length 522;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 490; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 33 SLCTWGYSSNTRFTITLNYKDPPLTGDEETLASGIYSGDLICILLODDIPAPNIPSSSTD 92
DB 33 SLCTWGYSSNTRFTITLNYKDPPLTGDEETLASGIYSGDLICILLODDIPAPNIPSSSTD 92
QY 93 SEHSSLQNNNEOPLATSSNOTSMODEQPSDSFOGQAQSGVWVNDMSMLGPSQNFEBASIQ 152
DB 93 SEHSSLQNNNEOPLATSSNOTSMODEQPSDSFOGQAQSGVWVNDMSMLGPSQNFEBASIQ 152
QY 153 DNAMHAGTGTFYPSPEPMUCSBSVSGVPHSLFTLYQSADCSANDALIVLHLMESGY 212
DB 153 DNAMHAGTGTFYPSPEPMUCSBSVSGVPHSLFTLYQSADCSANDALIVLHLMESGY 212
QY 213 IPQTEAKALSMPEKMLSGYKLYQYHPLCEGSSATLTCVPGNLIIVNATLKINNEIR 272
DB 213 IPQTEAKALSMPEKMLSGYKLYQYHPLCEGSSATLTCVPGNLIIVNATLKINNEIR 272
QY 273 SVKRLQLLPESFTCEKLGENVANITYDLOKLSLRFDOJLVPLAFTROALNLPDVFG 332
DB 273 SVKRLQLLPESFTCEKLGENVANITYDLOKLSLRFDOJLVPLAFTROALNLPDVFG 332
QY 333 VVLELELKLRIPLLDVRSVLSAVCRDLFTASNDPLMRFLYRDFRNTVAVQDTDM 392
DB 333 VVLELELKLRIPLLDVRSVLSAVCRDLFTASNDPLMRFLYRDFRNTVAVQDTDM 392
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QY 393 KELYRKHHIORKESPKGRFVWLLPSSSTHTTIPYPNPPLHPRPPSSRLPGIIGGEYDQRP 452
 Db 393 KELYRKHHIORKESPKGRFVWLLPSSSTHTTIPYPNPPLHPRPPSSRLPGIIGGEYDQRP 452
 QY 453 TLPVVGDPISSLIPGPGETPSQFPPLRRFPDVGPLPGPNPILPGRGGPNDRPFRPSRG 512
 Db 453 TLPVVGDPISSLIPGPGETPSQFPPLRRFPDVGPLPGPNPILPGRGGPNDRPFRPSRG 512
 QY 513 RPTDGRLSFM 522
 Db 513 RPTDGRLSFM 522

RESULT 5

AAW68521
 ID AAW68521 standard; protein; 591 AA.

AC AAW68521;

DT 25-JAN-1999 (first entry)

DE Human RIP-associated protein.

KM Human; RIP-associated protein; RAP; primer; PCR; amplification; probe;
 KM hybridisation; death domain; MORT MODULE; ICE-like family protease;
 KM kinase; TRAF domain; inflammation; cell death; tumour; HIV; infection.

OS Homo sapiens.

PN WO9841624-A1.

PD 24-SEP-1998.

PF 19-MAR-1998; 98MO-IL000125.

PR 19-MAR-1997; 97IL-00120485.

PA (YEDA) YEDA RES & DEV CO LTD.

PI Wallach D, Kovalenko A;

DR WPI; 1998-531565/45.

DR N-PSDB; AAV57200.

PT DNA encoding RIP-associated protein (RAP) - useful for, e.g. treatment of
 tumour cells or HIV-infected cells.

PS Claim 10; Fig 2; 65pp; English.

XX This sequence represent part of a human RIP-associated protein (RAP). The
 CC coding sequence was isolated from a B-cell library by a yeast 2-hybrid
 CC screen using the RIP protein devoid of its "death domain" as a bait. The
 CC screen isolated a clone of about 1.9 kb. Primers were generated based on
 CC the sequence and used to PCR amplify probes for screening a colon and
 CC heart cDNA library. A further 300 bp of sequence was determined, which
 CC was added to the 1.9 kb of sequence from the B-cell library. The encoded
 CC protein does not contain a "death domain", MORT MODULE, ICE-like family
 CC protease domain, kinase domain, nor TRAF domains. RAP was shown to bind
 CC only to RIP and not to TRADD, MORT-1, p55-R, p75-R or MACH. The protein
 CC can be used to modulate or mediate RIP modulated/mediated intracellular
 CC effects on the inflammation, cell death or cell survival pathways in
 CC which RIP is involved, e.g. for treating tumour cells or HIV-infected
 CC cells

XX Sequence 591 AA;

XX Query March 79.9%; Score 417; DB 2; Length 591;

XX Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Gaps 0;

QY Matches 417; Conservative 0; Indels 0; Gaps 0;

QY 106 LATSNQTSMDQEPSDSFGQAAQSGVWVNDMSLGPSCQNFEEASIQDNAMAREGTGFPY 165

Db 175 LATSNQTSMDQEPSDSFGQAAQSGVWVNDMSLGPSCQNFEEASIQDNAMAREGTGFPY 234
 QY 166 SEPMLCSSEVGEQVPHSLJETTLYQSADCSGANDALIVLTHLMLESQYIPQTEAKALSM 225
 Db 235 SEPMLCSSEVGEQVPHSLJETTLYQSADCSGANDALIVLTHLMLESQYIPQTEAKALSM 294
 QY 226 EKMKLSGYKKIQYHMLPLEGSSATLTCTVPLGNLVVNTAKINNEIRSVKRLQLPESFI 285
 Db 225 EKMKLSGYKKIQYHMLPLEGSSATLTCTVPLGNLVVNTAKINNEIRSVKRLQLPESFI 354
 QY 286 CEKLGENVANIYKDLQKLSRLFKDQLYPPLAFTROALNPVFGVVLPLELKLRIFR 345
 Db 355 CEKLGENVANIYKDLQKLSRLFKDQLYPPLAFTROALNPVFGVVLPLELKLRIFR 414
 QY 346 LIDVRSVLSLAVCRDLFTASNDPLWRFVLRDPRDNTVAVOOTDKELYRKHHIORKE 405
 Db 415 LIDVRSVLSLAVCRDLFTASNDPLWRFVLRDPRDNTVAVOOTDKELYRKHHIORKE 474
 QY 406 SPKGRFVWLLPSSSTHTTIPYPNPPLHPRPPSSRLPGIIGGEYDQRPILPVGDPISSLI 465
 Db 475 SPKGRFVWLLPSSSTHTTIPYPNPPLHPRPPSSRLPGIIGGEYDQRPILPVGDPISSLI 534
 QY 466 PGPGETPSQFPPLRRFPDVGPLPGPNPILPGRGGPNDRPFRPSRGPTDGRLSFM 522
 Db 535 PGPGETPSQFPPLRRFPDVGPLPGPNPILPGRGGPNDRPFRPSRGPTDGRLSFM 591

RESULT 6

AAAB35161
 ID AAB35161 standard; protein; 522 AA.

AC AAB35161;

DT 09-APR-2001 (first entry)

DE Human Skp1-associated F-box protein-1 SAF-1beta SEQ ID NO: 10.

KM Human; protein degradation; slah-mediated degradation protein; SMDP;
 KM SCF-complex protein; SCF; slah-1alpha; slah-1 interacting protein; SIP;
 KM Skp1-associated F-box protein; SAF-1; SAF-2; SMD; cancer; cell division;
 KM Skp1-associated destruction-box protein; inflammatory disease.

OS Homo sapiens.

PN WO200077207-A2.

PD 21-DEC-2000.

PF 09-JUN-2000; 2000MO-US015873.

PR 11-JUN-1999; 99US-0030517.

PA (BURN-) BURNHAM INST.

PI Reed JC, Matsuzawa S;

DR WPI; 2001-071273/08.

DR N-PSDB; AAC67285.

PT Slah-Mediated Degradation Protein, useful for drug screening, for
 therapeutic applications and for functional genomics.

PS Claim 15; Page 107-108; 121pp; English.

XX The present invention provides the protein and coding sequences of
 CC several slah-mediated degradation proteins and SCF-complex proteins.
 CC These are designated slah-1alpha, slah-1 interacting protein (SIP),
 CC which encodes two proteins due to alternative splicing (SIP-L and SIP-S). Skp1-
 CC associated F-box protein-1alpha and beta and -2 (SAF-1alpha, SAF-1beta
 CC and SAF-2) and Skp1-associated destruction-box protein (SMD). The
 CC proteins and their coding sequences are useful in the diagnosis and
 CC treatment of cancers, disorders where too little cell division occurs
 CC such as bone marrow aplasias, immunodeficiencies and inflammatory

CC diseases including sepsis, fibrosis, arthritis and graft versus host
CC disease
XX
SQ Sequence 522 AA;
Query Match 74.5%; Score 389; DB 4; Length 522;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 489; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 33 SLICTWGYSSNTRFTITLNYKDPPLTGDEETLASYGIVSGDLICILLODDIPAPNIPSSD 92
DB 33 SLICTWGYSSNTRFTITLNYKDPPLTGDEETLASYGIVSGDLICILLODDIPAPNIPSSD 92
QY 93 SEHSLQNNNEOPSLATSSNOTSNOTSODEPSPDSFOGQAAGSVMNDMSMLGSPQNEABSIQ 152
DB 93 SEHSLQNNNEOPSLATSSNOTSNOTSODEPSPDSFOGQAAGSVMNDMSMLGSPQNEABSIQ 152
QY 153 DNAMAGGTGFPYSEPMKCSSEVGVPHSLETLYQSGADSDANDALIVLHLMLESGY 212
DB 153 DNAMAGGTGFPYSEPMKCSSEVGVPHSLETLYQSGADSDANDALIVLHLMLESGY 212
QY 213 IPOGTEAKALSMPEKMKLSGYKLYQVHPLCEGSSATLTCVPLGNLIVNATLKINNEIR 272
DB 213 IPOGTEAKALSMPEKMKLSGYKLYQVHPLCEGSSATLTCVPLGNLIVNATLKINNEIR 272
QY 273 SVKRLQLLPESFTCKEKLGENVANITYKDLQKLSLTFKDLVYPLAFTROALNLPVFG 332
DB 273 SVKRLQLLPESFTCKEKLGENVANITYKDLQKLSLTFKDLVYPLAFTROALNLPVFG 332
QY 333 VVLPELKLRIFRLLDVRSVLSLSAVCRDLFTASNDPLMRFVLYLRDFRNTVAVODTW 392
DB 333 VVLPELKLRIFRLLDVRSVLSLSAVCRDLFTASNDPLMRFVLYLRDFRNTVAVODTW 392
QY 393 KELRKRIHOKKESPKGRFVWLTPSSSTHTTPEYFNPLHPPSPSSRLPGIIGEXDORP 452
DB 393 KELRKRIHOKKESPKGRFVWLTPSSSTHTTPEYFNPLHPPSPSSRLPGIIGEXDORP 452
QY 453 TLPRVGDPISSLLIPGEPSPSPPLRPRDPVGPLPGPNPLIGRGGPNDRPFRRSRG 512
DB 453 TLPRVGDPISSLLIPGEPSPSPPLRPRDPVGPLPGPNPLIGRGGPNDRPFRRSRG 512
QY 513 RPTGGRLSFM 522
DB 513 RPTGGRLSFM 522
RESULT 7
AAU32109 standard; protein; 607 AA.
XX
AC AAU32109;
XX
DT 18-DEC-2001 (first entry)
XX
DE Novel human secreted protein #2600.
XX
KW Human; vaccination; gene therapy; nutritional supplement;
KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200179449-A2.
XX
PD 25-OCT-2001.
XX
PF 16-APR-2001; 2001WO-US008656.
XX
PR 18-APR-2000; 2000US-00552929.
XX
PR 26-JAN-2001; 2001US-00770160.
XX
PA (HSE-) HSEQ INC.
XX

PI Tang YT, Liu C, Drenth RT;
XX
DR WPI; 2001-611725/70.
XX
XX
PT Nucleic acids encoding a range of human polypeptides, useful in genetic
PS vaccination, testing and therapy.
PS Claim 20; Page 556; 765pp; English.
XX
XX The invention relates to novel human secreted polypeptides. The
CC polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising the
CC nucleic acids encoding the polypeptides and cells genetically engineered
CC to express them are also useful for producing the proteins. The proteins
CC are useful in genetic vaccination, testing and therapy, and can be used
CC as nutritional supplements. They may be used to increase stem cell
CC proliferation, to regulate haematopoiesis, and in bone, cartilage, tendon
CC and/or nerve tissue growth or regeneration; immune suppression and/or
CC stimulation; as anti-inflammatory agents; and in treatment of leukaemia.
CC AAU29510-AAU33304 represent the amino acid sequences of novel human
CC secreted proteins of the invention
XX
SQ Sequence 607 AA;
Query Match 67.8%; Score 354; DB 4; Length 607;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 33 SLICTWGYSSNTRFTITLNYKDPPLTGDEETLASYGIVSGDLICILLODDIPAPNIPSSD 92
DB 33 SLICTWGYSSNTRFTITLNYKDPPLTGDEETLASYGIVSGDLICILLODDIPAPNIPSSD 127
QY 68 SEHSLQNNNEOPSLATSSNOTSNOTSODEPSPDSFOGQAAGSVMNDMSMLGSPQNEABSIQ 152
DB 68 SEHSLQNNNEOPSLATSSNOTSNOTSODEPSPDSFOGQAAGSVMNDMSMLGSPQNEABSIQ 187
QY 128 SEHSLQNNNEOPSLATSSNOTSNOTSODEPSPDSFOGQAAGSVMNDMSMLGSPQNEABSIQ 187
DB 128 SEHSLQNNNEOPSLATSSNOTSNOTSODEPSPDSFOGQAAGSVMNDMSMLGSPQNEABSIQ 187
QY 153 DNAMAGGTGFPYSEPMKCSSEVGVPHSLETLYQSGADSDANDALIVLHLMLESGY 212
DB 153 DNAMAGGTGFPYSEPMKCSSEVGVPHSLETLYQSGADSDANDALIVLHLMLESGY 247
QY 213 IPOGTEAKALSMPEKMKLSGYKLYQVHPLCEGSSATLTCVPLGNLIVNATLKINNEIR 272
DB 213 IPOGTEAKALSMPEKMKLSGYKLYQVHPLCEGSSATLTCVPLGNLIVNATLKINNEIR 307
QY 273 SVKRLQLLPESFTCKEKLGENVANITYKDLQKLSLTFKDLVYPLAFTROALNLPVFG 332
DB 273 SVKRLQLLPESFTCKEKLGENVANITYKDLQKLSLTFKDLVYPLAFTROALNLPVFG 367
QY 333 VVLPELKLRIFRLLDVRSVLSLSAVCRDLFTASNDPLMRFVLYLRDFRNTVAVODTW 421
DB 333 VVLPELKLRIFRLLDVRSVLSLSAVCRDLFTASNDPLMRFVLYLRDFRNTVAVODTW 421
RESULT 8
AAB35160 standard; protein; 443 AA.
XX
AC AAB35160;
XX
DT 09-APR-2001 (first entry)
XX
DE Human Skp1-associated F-box protein-1 SAF-1alpha SEQ ID NO: 8.
XX
KW Human; protein degradation; shah-mediated degradation protein; SMDP;
KW SCF-complex protein; SCP; shah-1alpha; shah-1 interacting protein; SIP;
KW Skp1-associated F-box protein; SAF-1; SAF-2; SMD; cancer; cell division;
KW Skp1-associated destruction-box protein; inflammatory disease.
XX

OS Homo sapiens.
 XX WO20007207-A2.
 XX 21-DEC-2000.
 XX 09-JUN-2000; 2000WO-US015873.
 XX 11-JUN-1999; 99US-00330517.
 XX (BURN-) BURNHAM INST.
 PA Reed JC, Matsuzawa S;
 PI WPI; 2001-071273/08.
 DR N-PSDB; AAC67284.
 XX
 XX Slah-mediated Degradation Protein, useful for drug screening, for
 PT therapeutic applications and for functional genomics.
 XX
 PS Claim 15; Page 103-104; 121pp; English.
 XX
 CC The present invention provides the protein and coding sequences of
 CC several slah-mediated degradation proteins and SCF-complex proteins.
 CC These are designated Slah-1alpha, Slah-1 interacting protein (SIP), which
 CC encodes two proteins due to alternative splicing (SIP-L and SIP-S), Skp1-
 CC associated F-box protein-1alpha and beta and -2 (SAF-1alpha, SAF-1beta
 CC and SAF-2) and Skp1-associated destruction-box protein (SAB). The
 CC proteins and their coding sequences are useful in the diagnosis and
 CC treatment of cancers, disorders where too little cell division occurs
 CC such as bone marrow aplasia, immunodeficiencies and inflammatory
 CC diseases including sepsis, fibrosis, arthritis and graft versus host
 CC disease
 XX
 XX Sequence 443 AA;
 SQ
 Query Match 63.2%; Score 330; DB 4; Length 443;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 430; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 92 DSEHSSIQNNEQPSLATSNQTSNQBQPSDFQGAAGGVNDDSMGLPSONFAESI 151
 DB 13 DSEHSSIQNNEQPSLATSNQTSNQBQPSDFQGAAGGVNDDSMGLPSONFAESI 72
 QY 152 QDNAMHAEAGTFPSEBMLCSSEVGEQVPHSLTLVQASDANALTLHLMLSEG 211
 DB 73 QDNAMHAEAGTFPSEBMLCSSEVGEQVPHSLTLVQASDANALTLHLMLSEG 132
 QY 212 YIPQGTAKALSMPEKMKLSGVYKLYQYHPLCEGSSATLTCVPLGNLIVNATLKINNEI 271
 DB 133 YIPQGTAKALSMPEKMKLSGVYKLYQYHPLCEGSSATLTCVPLGNLIVNATLKINNEI 192
 QY 272 RSVKRLQOLPESFICKKRGENTANYKDIQKSRFLFKQOLVYPLAFTQALNLDVVG 331
 DB 193 RSVKRLQOLPESFICKKRGENTANYKDIQKSRFLFKQOLVYPLAFTQALNLDVVG 252
 QY 332 LVVLPLELTKIRIFRLDVRSGVLSLAVCRDLFTASNDPLMRFLYRDFPDNTVRQDDND 391
 DB 253 LVVLPLELTKIRIFRLDVRSGVLSLAVCRDLFTASNDPLMRFLYRDFPDNTVRQDDND 312
 QY 392 WKELYRKRAHQKESPKGRFVNLIPSTHTIPYPNHLHPRPPSSRLPGLIGGEYDOR 451
 DB 313 WKELYRKRAHQKESPKGRFVNLIPSTHTIPYPNHLHPRPPSSRLPGLIGGEYDOR 372
 QY 452 PTLPYVADPISLIPGGETPSPQPLPRPFDVGPPLPGNPPLIPRGGGNDPFRPBR 511
 DB 373 PTLPYVADPISLIPGGETPSPQPLPRPFDVGPPLPGNPPLIPRGGGNDPFRPBR 432
 QY 512 GRPTDGLSLFM 522
 DB 433 GRPTDGLSLFM 443

RESULT 9
 ABB90108
 ID ABB90108 standard; protein; 317 AA.
 XX
 AC ABB90108;
 XX
 DT 24-MAY-2002 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 2484.
 XX
 XX Cytostatic; immunosuppressive; nocotropic; neuroprotective; antiviral;
 XX anti-allergic; hepatocytotoxic; antidiabetic; anti-inflammatory; antiviral;
 XX vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;
 XX cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
 XX neurological disease; infection; human; secreted protein.
 XX
 OS Homo sapiens.
 XX
 XX WO200190304-A2.
 XX
 XX 29-NOV-2001.
 XX
 XX 18-MAY-2001; 2001WO-US016450.
 XX
 XX 19-MAY-2000; 2000US-0205515P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Birse CE, Rosen CA;
 PI WPI; 2002-122018/16.
 DR N-PSDB; ABL90517.
 XX
 XX Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
 PT prevention of neural, immune system, muscular, reproductive,
 PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
 PT disorders.
 XX
 PS Claim 11; SEQ ID NO 2484; 2081pp + Sequence Listing; English.
 XX
 CC The invention relates to novel genes (ABL9449-ABJ90853) and proteins
 CC (ABB89040-ABB90444) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
 CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
 CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
 CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
 CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
 CC infectious diseases such as viral, bacterial, fungal and parasitic
 CC infections. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SO Sequence 317 AA;
 Query Match 51.9%; Score 271; DB 5; Length 317;
 Best Local Similarity 100.0%; Pred. No. 4.6e-262;
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 140 LGPSONFAESIQDNAMHAEAGTFPSEBMLCSSEVGEQVPHSLTLVQASDANAL 199
 DB 26 LGPSONFAESIQDNAMHAEAGTFPSEBMLCSSEVGEQVPHSLTLVQASDANAL 85
 QY 200 IVLHILMLSEGYYIPQGTAKALSMPEKMKLSGVYKLYQYHPLCEGSSATLTCVPLGNLI 259
 DB 86 IVLHILMLSEGYYIPQGTAKALSMPEKMKLSGVYKLYQYHPLCEGSSATLTCVPLGNLI 145
 QY 260 VVATLTKINNEIRSVKRLQOLPESFICKKRGENTANYKDIQKSRFLFKQOLVYPLAFT 319

DB 146 VVNTIKNNIRSVKQLLPESFICKKNGENVNIYDLOQLSLFPDQVYPLAF 205
 QY 320 TRQALNPDVFGVLVPLELKLRIFFRLLDVRSVLSAVCRDLFTASNDPLMRFLYLRD 379
 DB 206 TRQALNPDVFGVLVPLELKLRIFFRLLDVRSVLSAVCRDLFTASNDPLMRFLYLRD 265
 QY 380 FRDNTVRVQDTPDKELVYRKHIORKESPGR 410
 DB 266 FRDNTVRVQDTPDKELVYRKHIORKESPGR 296

RESULT 10
 ADJ68946
 ID ADJ68946 standard; protein; 221 AA.
 AC ADJ68946;
 DT 06-MAY-2004 (first entry)
 DE Human heat mitochondrial protein as a therapeutic target SeqID752.
 XX
 KW Mitochondrial; human; screening assay; diabetes mellitus;
 KW Huntington's disease; osteoarthritis;
 KW Leber's hereditary optic neuropathy; LHON;
 KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
 KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
 KW neuroprotective; noctropic; antidiabetic; anticonvulsant; antiarthritic;
 KW osteopathic; ophthalmological; cytosstatic.
 XX
 OS Homo sapiens.
 PN WO2003087768-A2.
 XX
 PD 23-OCT-2003.
 PF 04-APR-2003; 2003WO-US010870.
 XX
 PR 12-APR-2002; 2002US-0372843P.
 PR 17-JUN-2002; 2002US-0389987P.
 PR 20-SEP-2002; 2002US-0412418P.
 XX
 PA (MITO-) MITOKOR.
 PA (BUCK-) BUCK INST AGE RES.
 PI Ghosh SS, Fathy ED, Zhang B, Gibson BW, Taylor SW, Glenn GW;
 PI Warnock DE;
 DR WPI; 2003-845369/78.
 XX
 PT Identifying a mitochondrial target for drug screening assays and for
 PT treating diseases associated with altered mitochondrial function;
 PT comprises detecting a modified polypeptide in a sample and correlating
 PT with the disease.
 XX
 PS Claim 1; SEQ ID NO 752; 180dp; English.
 XX
 CC This invention relates to novel mitochondrial targets that can be used
 CC for therapeutic intervention in treating a disease associated with
 CC altered mitochondrial function. Specifically, it refers to a method for
 CC identifying proteins of the human heat mitochondrial proteome that are
 CC useful for drug screening assays, as well as therapeutic targets. The
 CC present invention describes a method for identifying such proteins that
 CC can be used in the treatment of various diseases associated with altered
 CC mitochondrial function including diabetes mellitus, Huntington's disease,
 CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
 CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
 CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
 CC compositions have neuroprotective, noctropic, antidiabetic,
 CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
 CC cytosstatic activities. This polypeptide sequence is a human heart
 CC mitochondrial protein of the invention.

SQ Sequence 221 AA;
 Query Match 44.3%; Score 221; DB 7; Length 221;
 Best Local Similarity 100.0%; Pred No. 3,7e-222;
 Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 ENVANIYKLOQLSLFPDQVYPLAFTRQALNPDVFGVLVPLELKLRIFFRLLDVRS 351
 DB 1 ENVANIYKLOQLSLFPDQVYPLAFTRQALNPDVFGVLVPLELKLRIFFRLLDVRS 60
 QY 352 VLSAVCRDLFTASNDPLMRFLYLRDPRONTVRVQDTPDKELVYRKHIORKESPGRF 411
 DB 61 VLSAVCRDLFTASNDPLMRFLYLRDPRONTVRVQDTPDKELVYRKHIORKESPGRF 120
 QY 412 VMLPSSHTTIPFYENPLHPRFPSSRLPPGIIGGYDQRPPLPYGDPISLLIPGGET 471
 DB 121 VMLPSSHTTIPFYENPLHPRFPSSRLPPGIIGGYDQRPPLPYGDPISLLIPGGET 180
 QY 472 PSQFPPLRRPDVGPVPLPGPNPILPGRGPNDRFPFRSRGRPTDGRLSFM 522
 DB 181 PSQFPPLRRPDVGPVPLPGPNPILPGRGPNDRFPFRSRGRPTDGRLSFM 221

RESULT 11
 ADJ54155
 ID ADJ54155 standard; protein; 221 AA.
 AC ADJ54155;
 DT 20-NOV-2003 (first entry)
 DE Human protein, SEQ ID 1723.
 XX
 KW Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Noctropic;
 KW Gene Therapy; human; secretory protein; membrane proteins; cancer;
 KW inflammatory disease; osteoporosis; neurological disease.
 XX
 OS Homo sapiens.
 PN EP1293569-A2.
 XX
 PD 19-MAR-2003.
 PF 21-MAR-2002; 2002EP-00006586.
 XX
 PR 14-SEP-2001; 2001JP-00328381.
 PR 24-JAN-2002; 2002US-0350435P.
 XX
 PA (HELI-) HELIX RES INST.
 PA (REAS-) RES ASSOOC BIOTECHNOLOGY.
 PI Isogai T, Sugiyama T, Otsuki T, Makamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Maehuo Y;
 DR WPI; 2003-395539/38.
 DR N-PSDB; ADA52516.
 XX
 PT New polynucleotides encoding full-length polypeptides, e.g. secretory
 PT and/or membrane proteins, useful for developing medicines for diseases in
 PT which the gene is involved, or as target molecules for gene therapy.
 XX
 PS Claim 14; SEQ ID NO 1723; 205dp; English.
 XX
 CC The present invention relates to novel human secretory or membrane
 CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-
 CC ADA54071). The coding sequences are useful in the gene therapy of
 CC diseases caused by abnormalities of the proteins, e.g. cancer,
 CC inflammatory diseases, osteoporosis or neurological disease.

SQ Sequence 221 AA;
 Query Match 38.3%; Score 200; DB 6; Length 221;

Best Local Similarity 100.0%; Pred. No. 3.8e-191; Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 323 ALNLPDVGVLVLELKLRIFFRLDVRVLSLSAVCRDLFTASNDPLMRELYLRDFRD 382
 Db 22 ALNLPDVGVLVLELKLRIFFRLDVRVLSLSAVCRDLFTASNDPLMRELYLRDFRD 81
 QY 363 NTVRVQDTWKELVRRKHIOKESPKGRFVWLLPSSHTIIPFYNPPLHRRPFPSSRLPPG 442
 Db 82 NTVRVQDTWKELVRRKHIOKESPKGRFVWLLPSSHTIIPFYNPPLHRRPFPSSRLPPG 141
 QY 443 IIGGEYDQRPFLPYVGDPISSLLPGGETPSQFPPLRPRFDPVGLPGNPILPGRCGPN 502
 Db 142 IIGGEYDQRPFLPYVGDPISSLLPGGETPSQFPPLRPRFDPVGLPGNPILPGRCGPN 201
 QY 503 DRPFPRPSRGRPTDGRLSFM 522
 Db 202 DRPFPRPSRGRPTDGRLSFM 221

RESULT 12

ABB90109 standard; protein; 462 AA.

AC ABB90109;
 XX
 XX 24-MAY-2002 (first entry)

DE Human polypeptide SEQ ID NO 2485.

XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
 KW anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; anticancer;
 KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;
 KW cardiac; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein.

OS Homo sapiens.

PN WO200190304-A2.

PD 29-NOV-2001.

PF 18-MAY-2001; 2001WO-US016450.

XX 19-MAY-2000; 2000US-0205515P.

XX (HUMA-) HUMAN GENOME SCI INC.

PI Birse CE, Rosen CA;

XX WPI; 2002-122018/16.

DR N-PSDB; ABL90518.

XX Novel 1405 isolated polypeptides, useful for diagnosis, treatment and

PT prevention of neural immune system, muscular, reproductive,

PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative

PT disorders.

XX Claim 11; SEQ ID NO 2485; 2061pp + Sequence Listing; English.

XX The invention relates to novel genes (ABL89449-ABL90853) and proteins
 CC (ABB9040-ABB90444) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
 CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
 CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
 CC disorders e.g. Addison's disease, allergies, autoimmune hemolytic
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
 CC cardiovascular disorders such as myocardial ischemias; (d) wound healing
 CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)

CC infectious diseases such as viral, bacterial, fungal and parasitic
 CC infections. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at [ftp://wipo.int/pub/published_pcl_sequences](http://wipo.int/pub/published_pcl_sequences)
 XX SQ Sequence 462 AA;

Query Match 38.3%; Score 200; DB 5; Length 462;
 Best Local Similarity 100.0%; Pred. No. 7.3e-191; Indels 0; Gaps 0;
 Matches 200; Conservative 0; Mismatches 0;

QY 323 ALNLPDVGVLVLELKLRIFFRLDVRVLSLSAVCRDLFTASNDPLMRELYLRDFRD 382
 Db 263 ALNLPDVGVLVLELKLRIFFRLDVRVLSLSAVCRDLFTASNDPLMRELYLRDFRD 322
 QY 383 NTVRVQDTWKELVRRKHIOKESPKGRFVWLLPSSHTIIPFYNPPLHRRPFPSSRLPPG 442
 Db 323 NTVRVQDTWKELVRRKHIOKESPKGRFVWLLPSSHTIIPFYNPPLHRRPFPSSRLPPG 382
 QY 443 IIGGEYDQRPFLPYVGDPISSLLPGGETPSQFPPLRPRFDPVGLPGNPILPGRCGPN 502
 Db 383 IIGGEYDQRPFLPYVGDPISSLLPGGETPSQFPPLRPRFDPVGLPGNPILPGRCGPN 442
 QY 503 DRPFPRPSRGRPTDGRLSFM 522
 Db 443 DRPFPRPSRGRPTDGRLSFM 462

RESULT 13

ADA57586 standard; protein; 462 AA.

AC ADA57586;

XX 20-NOV-2003 (first entry)

DE Human secreted protein #566.

XX immunosuppressive; anti-inflammatory; antiallergic;
 KW cytosolic; cerebroprotective; neuroprotective; nootropic;
 KW cardiovascular; antiarteriosclerotic; gene therapy;
 KW human secreted protein; immune disorder; inflammation;
 KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;
 KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;
 KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;
 KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;
 KW triple helix formation; antisense gene therapy; forensic biology.

OS Homo sapiens.

PN WO2002102994-A2.

PD 27-DEC-2002.

PF 19-MAR-2002; 2002WO-US008278.

XX 21-MAR-2001; 2001US-0277340P.

XX 19-JUL-2001; 2001US-0306171P.

XX 13-NOV-2001; 2001US-0331287P.

XX (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Ruben SM;

XX WPI; 2003-167512/16.

DR N-PSDB; ADA56693.

XX New human secreted polypeptides and polynucleotides, useful for

PT diagnosing, treating or preventing e.g. immune disorders, inflammatory

PT conditions, respiratory disorders, cancers, CNS disorders, or

PT neurodegenerative disorders.

XX The invention relates to 592 new human secreted polypeptides useful for
CC diagnosing, treating or preventing e.g. immune disorders, inflammatory
CC conditions, respiratory disorders, cancers, CNS disorders, or
CC neurodegenerative disorders, or polypeptides comprising an amino acid
CC sequence at least 95% identical to the new sequences. The polypeptides,
CC antibodies or antibody fragments that bind to the polypeptides, nucleic
CC acids encoding the polypeptides, agonists or antagonists that binds to
CC the polypeptide, are useful in preparing diagnostic or pharmaceutical
CC compositions for diagnosing, treating or preventing an e.g. immune
CC disorders, inflammatory conditions (e.g. inflammatory bowel disease,
CC nephritis or Crohn's disease), respiratory disorders (e.g. asthma and
CC allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
CC (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative
CC disorders (e.g. Parkinson's disease or Alzheimer's disease), and
CC cardiovascular disorders (e.g. atherosclerosis or myocarditis). The
CC polynucleotides are useful for chromosome identification, chromosome
CC mapping, for controlling gene expression through triple helix formation
CC or antisense DNA or RNA, in gene therapy, for identifying individuals
CC from minute biological samples, in forensic biology and as hybridization
CC probes. The polypeptides are useful for as molecular weight markers on
CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
CC gels, to raise antibodies, for testing biological activities, and for
CC treating or preventing neural disorders, immune system disorders,
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC renal, proliferative and/or cancerous diseases. This sequence corresponds
CC to one of the polypeptide of the invention. Note: The sequence data for
CC this patent did form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 462 AA;

Query Match 38.3%; Score 200; DB 6; Length 462;

Best Local Similarity 100.0%; Pred. NO. 7.3e-191; Indels 0; Gaps 0;

Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 323 ALNLPDVGVLVPLELKLRIFFLLDVRSVLSAVCRDFTASNDPLMRFYLYRDFRD 382
DB 263 ALNLPDVGVLVPLELKLRIFFLLDVRSVLSAVCRDFTASNDPLMRFYLYRDFRD 322
QY 383 NTAVVQOTDWEKELRKHHIQKESPKRFPWLLPSSHTTTPFYNPPLHPRFPSSRLPPG 442
DB 323 NTAVVQOTDWEKELRKHHIQKESPKRFPWLLPSSHTTTPFYNPPLHPRFPSSRLPPG 382
QY 443 IIGGEYDORPPLPYVGPDISLIPGPGTSPQFPPLRPRDPVGLPGPNILPGRGPN 502
DB 383 IIGGEYDORPPLPYVGPDISLIPGPGTSPQFPPLRPRDPVGLPGPNILPGRGPN 442
QY 503 DRFPFRSGRGRPTDGRLSFM 522
DB 443 DRFPFRSGRGRPTDGRLSFM 462

RESULT 14

ADA41482
ID ADA41482 standard; protein, 462 AA.

XX ADA41482;

DT 20-NOV-2003 (first entry)

XX Human secreted protein.

XX Human, secreted protein; cancer; hyperproliferative disorder;

XX rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;

XX wound healing; cytostatic; immunosuppressive; nootropic; neuroprotective;

XX antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory;

XX vulnary; cardiac; gene therapy.

XX Homo sapiens.

XX

PN WO2002102993-A2.
XX
XX 27-DEC-2002.
XX
XX 19-MAR-2002; 2002MO-US008123.
XX
XX 21-MAR-2001; 2001US-027344P.
XX 19-JUL-2001; 2001US-0306171P.
XX 13-NOV-2001; 2001US-0331287P.
XX (HUMA-1) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM;
XX WPL, 2003-175238/17.
XX
XX New human secreted proteins and nucleic acid molecules, useful for
XX preparing a diagnostic or pharmaceutical composition for diagnosing,
XX preventing or treating cancer or other hyperproliferative disorder,
XX asthma, allergies or AIDS.

Claim 1; SEQ ID NO 1865; 3205pp; English.

XX The invention relates to novel genes ADA39629-ADA40565 and proteins
XX ADA40566-ADA41501 for human secreted proteins, useful for preventing,
XX treating or ameliorating medical conditions e.g. by protein or gene
XX therapy. The polypeptides, nucleic acid molecules, antibodies or their
XX fragments, and agonists or antagonists that bind to the polypeptide are
XX useful for preparing a diagnostic or pharmaceutical composition for
XX diagnosing or treating cancer or other hyperproliferative disorder. The
XX polypeptides and nucleic acid molecules are also useful for detecting,
XX preventing, diagnosing, prognosticating, treating or ameliorating cancer
XX or other hyperproliferative disorders including neoplasms, autoimmune
XX disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus
XX erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic
XX anaemia), haematopoietic or hematological disorders (e.g. anaemia,
XX thrombocytopenia), allergic reactions including asthma or eczema,
XX inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory
XX bowel disease or Crohn's disease), neurodegenerative disorders (e.g.
XX Alzheimer's disease or Parkinson's disease), cardiovascular disorders
XX (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,
XX fungal or viral infections including HIV/AIDS), or wound healing and
XX disorders of epithelial cell proliferation. The nucleic acids are also
XX useful for chromosome identification, radiation hybrid mapping or long-
XX range restriction mapping, as molecular weight markers, or as
XX hybridization or diagnostic probes. The polypeptides and antibodies are
XX useful for providing immunohistochemistry assays. Note: The sequence data for
XX of the tissues immunohistochemistry assays. Note: The sequence data for
XX this patent did not form part of the printed specification, but was
XX obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 462 AA;

Query Match 38.3%; Score 200; DB 6; Length 462;

Best Local Similarity 100.0%; Pred. NO. 7.3e-191; Indels 0; Gaps 0;

Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 323 ALNLPDVGVLVPLELKLRIFFLLDVRSVLSAVCRDFTASNDPLMRFYLYRDFRD 382
DB 263 ALNLPDVGVLVPLELKLRIFFLLDVRSVLSAVCRDFTASNDPLMRFYLYRDFRD 322
QY 383 NTAVVQOTDWEKELRKHHIQKESPKRFPWLLPSSHTTTPFYNPPLHPRFPSSRLPPG 442
DB 323 NTAVVQOTDWEKELRKHHIQKESPKRFPWLLPSSHTTTPFYNPPLHPRFPSSRLPPG 382
QY 443 IIGGEYDORPPLPYVGPDISLIPGPGTSPQFPPLRPRDPVGLPGPNILPGRGPN 502
DB 383 IIGGEYDORPPLPYVGPDISLIPGPGTSPQFPPLRPRDPVGLPGPNILPGRGPN 442
QY 503 DRFPFRSGRGRPTDGRLSFM 522
DB 443 DRFPFRSGRGRPTDGRLSFM 462

RESULT 15
ABR48139
ID ABR48139 standard; protein; 462 AA.
XX
AC ABR48139;
XX
DT 12-JUN-2003 (first entry)
XX
DE Human secreted protein, SEQ ID 1030.
XX
KW Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic;
KW vulnary; antiinflammatory; nootropic; neuroprotective;
KW antiparkinsonian; gene therapy; human; cardiovascular disorder.
XX
OS Homo sapiens.
XX
PN MO200295010-A2.
XX
PD 28-NOV-2002.
XX
PF 19-MAR-2002; 2002WO-US009785.
XX
PR 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR MPI, 2003-129429/12.
XX
PT Novel human secreted proteins, useful for detecting, preventing,
PT diagnosing, prognosticating, treating and/or ameliorating cardiovascular
PT disorders such as arrhythmia.
XX
PS Claim 13; SEQ ID NO 1030; 1881pp; English.
XX
CC The present invention relates to novel human secreted proteins (ABR47633-
CC ABR48145) and their coding sequences (ACC50344-ACC50856). The proteins
CC and their coding sequences are useful for the preparation of a diagnostic
CC or pharmaceutical composition for diagnosing or treating a cardiovascular
CC disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary
CC arteriosclerosis and myocardial ischaemia), neural disorders, immune
CC system disorders, muscular disorders, reproductive disorders,
CC gastrointestinal disorders, pulmonary disorders, renal disorders,
CC proliferative disorders and/or cancerous diseases and conditions, for
CC wound healing and epithelial cell proliferation, to treat inflammation or
CC infection, for treating thrombosis and arteriosclerosis, for treating or
CC preventing neural damage which occurs in neuronal disorders or
CC neurodegenerative conditions such as Alzheimer's disease and Parkinson's
CC disease, to enhance bone and periodontal regeneration and aid in tissue
CC transplants or bone grafts, to prevent skin aging or hair loss, to
CC stimulate growth and differentiation of haematopoietic cells and bone
CC marrow cells when used in combination with other cytokines, to maintain
CC organs before transplantation or for supporting cell culture of primary
CC tissues, to increase or decrease differentiation or proliferation of
CC embryonic stem cells, or to modulate mammalian characteristics or
CC metabolism. Note: The sequence data for this patent was published in
CC electronic format and is available from WIPO at
CC ftp.wipo.int/pub/published_pot_sequences
XX
SQ Sequence 462 AA;

Query Match 38.3%; Score 200; DB 6; Length 462;
Best Local Similarity 100.0%; Pred. No. 7.3e-191;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 323 ALNLDPVFGVLVPLELKLKIFRLLDVRSVLSASACRDIFTSNDPLIMRPLVLRDPD 382
DB 263 ALNLDPVFGVLVPLELKLKIFRLLDVRSVLSASACRDIFTSNDPLIMRPLVLRDPD 322

QY 383 NTVRVQDTDWKELYRKHHIQRKESPKGRFVMLPSSSTHTIPEYPNPLHRRPFPSSRLPPG 442
DB 323 NTVRVQDTDWKELYRKHHIQRKESPKGRFVMLPSSSTHTIPEYPNPLHRRPFPSSRLPPG 382
QY 443 IIGGEYDQRPPTLPYVGDPLISLLPGGETPSGPPPLRPREDPVGPLPGPPVPLPGRGPN 502
DB 383 IIGGEYDQRPPTLPYVGDPLISLLPGGETPSGPPPLRPREDPVGPLPGPPVPLPGRGPN 442
QY 503 DRPFPRPSRGRPTDGRLSFM 522
DB 443 DRPFPRPSRGRPTDGRLSFM 462

RESULT 16
ADC74596
ID ADC74596 standard; protein; 462 AA.
XX
AC ADC74596;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human secreted protein - SEQ ID 1229.
XX
KW antianaemic; antirheumatic; antiarrhythmic; antiinflammatory; antithyroid;
KW antidiabetic; immunosuppressive; dermatological; nephrotoxic;
KW antiparkinsonian; neuroprotective; nootropic; antibacterial; vitruide;
KW fungicide; antiparasitic; antiarteriosclerotic; vulnary; cytostatic;
KW haemopoietic; haematologic; anaemia; autoimmune disorder;
KW rheumatoid arthritis; inflammation; Grave's disease; diabetes;
KW systemic lupus erythematosus; glomerulonephritis; neurodegenerative;
KW Parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis;
KW cancer; bacterial; viral; fungal; parasitic infection; gene therapy;
KW human.
XX
OS Homo sapiens.
XX
PN MO2003038063-A2.
XX
PD 08-MAY-2003.
XX
PF 19-MAR-2002; 2002WO-US008277.
XX
PR 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR MPI, 2003-430516/40.
XX
DR N-PSDB; ADC73981.
XX
PT New human secreted polypeptide for diagnosing, preventing or treating
PT hematopoietic or hematologic disorders (e.g. anemia), autoimmune
PT disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer or
PT atherosclerosis).
XX
PS Claim 16; SEQ ID NO 1229; 2272pp; English.
XX
CC The invention relates to a novel human secreted polypeptide comprising a
CC defined sequence given in the specification. The polypeptide, nucleic
CC acid molecule, antibody, agonist or antagonist of the invention may be
CC useful for preparing a composition for diagnosing or treating a
CC haemopoietic or haematologic disorder such as anaemia, autoimmune
CC disorders such as rheumatoid arthritis, inflammation, Grave's disease,
CC diabetes, systemic lupus erythematosus or glomerulonephritis,
CC neurodegenerative disorders including Parkinson's disease and Alzheimer's
CC disease, wounds and hyperproliferative disorders including
CC atherosclerosis or cancer, as well as bacterial, viral, fungal or
CC parasitic infections. The polypeptide may also be used during gene
CC therapy procedures and for identifying a binding partner by contacting

CC the polypeptide with a binding partner and determining whether the
CC binding partner increases or decreases the activity of the polypeptide.
CC the current sequence is that of the human secreted protein of the
CC invention.
XX
SQ Sequence 462 AA;
Query Match 38 3%; Score 200; DB 7; Length 462;
Best Local Similarity 100.0%; Pred. No. 7.3e-191;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 323 ALNLPDVGVLVPLELKLRIPLLDVRSVLSAVCRDLFTASNDPLIMRPLYLDFPD 382
DB 263 ALNLPDVGVLVPLELKLRIPLLDVRSVLSAVCRDLFTASNDPLIMRPLYLDFPD 322
QY 383 NTRVVOPTDMKELRYRKHIOKESPKGRFVMLLPSTHTIPFPNPLHRRPPSSSLPFG 442
DB 323 NTRVVOPTDMKELRYRKHIOKESPKGRFVMLLPSTHTIPFPNPLHRRPPSSSLPFG 382
QY 443 IIGGEYQRFPLTPYVGPPISSLIPGQETPSQFPPLRPREDPYGPPGPPILPGSGGN 502
DB 383 IIGGEYQRFPLTPYVGPPISSLIPGQETPSQFPPLRPREDPYGPPGPPILPGSGGN 442
QY 503 DRPFPRSGRPFDDGRISFM 522
DB 443 DRPFPRSGRPFDDGRISFM 462
RESULT 17
ABG18510
ID ABG18510 standard; protein; 549 AA.
XX
AC ABG18510;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #18501.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN W0200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
XX
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Dermanac RT, Liu C, Tang YT;
XX
DR WPI: 2001-639362/73.
DR N-PSDB; AAS82697.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 48869; 103bp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is

CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pcr_sequences
XX
SQ Sequence 549 AA;
Query Match 25.7%; Score 134; DB 4; Length 549;
Best Local Similarity 100.0%; Pred. No. 9.6e-125;
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 33 SLCTWGYSSNTRTITLNYKDPYLTGDEETLASGYISGLICLIODDIPAPYIPSTSD 92
DB 34 SLCTWGYSSNTRTITLNYKDPYLTGDEETLASGYISGLICLIODDIPAPYIPSTSD 93
QY 93 SEHSSLQNNQPSLATSSNQTSMDQPSDFQGOAAQSGVWDDSMIGSPQNFEEASIQ 152
DB 94 SEHSSLQNNQPSLATSSNQTSMDQPSDFQGOAAQSGVWDDSMIGSPQNFEEASIQ 153
QY 153 DNAMHAEQTGYPS 166
DB 154 DNAMHAEQTGYPS 167
RESULT 18
ADA57587
ID ADA57587 standard; protein; 174 AA.
XX
AC ADA57587;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human secreted protein #566.
XX
KW immunosuppressive; antiinflammatory; antisthmatic; anti-allergic;
KW cyclostatic; cerebroprotective; neuroprotective; nocotropic;
KW cardiovascular; antiarteriosclerotic; gene therapy;
KW human secreted protein; immune disorder; inflammation;
KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;
KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;
KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;
KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;
KW triple helix formation; antisense gene therapy; forensic biology.
XX
OS Homo sapiens.
XX
PN W02002102994-A2.
XX
PD 27-DEC-2002.
XX
PF 19-MAR-2002; 2002WO-US008278.
XX
PR 21-MAR-2001; 2001US-0277340P.
XX
PR 19-JUN-2001; 2001US-0306171P.
XX
PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI: 2003-167512/16.
DR N-PSDB; ADA56694.
XX

RESULT 20
ABR48140
ID ABR48140 standard; protein; 174 AA.
XX
XX
AC ABR48140;
XX
XX
DT 12-JUN-2003 (first entry)
XX
DE Human secreted protein, SEQ ID 1031.
XX
XX
KW Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cyostatic;
KW vulnerary; antiinflammatory; nootropic; neuroprotective;
KW antiparkinsonian; gene therapy; human; cardiovascular disorder.
XX
OS Homo sapiens.
XX
PN WO200295010-A2.
XX
XX
PD 28-NOV-2002.
XX
XX
PF 19-MAR-2002; 2002MO-US009785.
XX
XX
PR 21-MAR-2001; 2001US-0277340P.
XX
PR 19-JUL-2001; 2001US-0306171P.
XX
PR 13-NOV-2001; 2001US-0331287P.
XX
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX
PI Rosen CA, Ruben SM;
XX
XX
DR WPI; 2003-129429/12.
XX
XX
PT Novel human secreted proteins, useful for detecting, preventing,
PT diagnosing, prognosticating, treating and/or ameliorating cardiovascular
PT disorders such as arrhythmia.
XX
XX
PS Claim 13; SEQ ID NO 1031; 1881bp; English.
XX
XX
CC The present invention relates to novel human secreted proteins (ABR47633-
CC ABR48145) and their coding sequences (ACC50344-ACC50856). The proteins
CC and their coding sequences are useful for the preparation of a diagnostic
CC or pharmaceutical composition for diagnosing or treating a cardiovascular
CC disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary
CC arteriosclerosis and myocardial ischaemia), neural disorders, immune
CC system disorders, muscular disorders, reproductive disorders,
CC gastrointestinal disorders, pulmonary disorders, renal disorders,
CC proliferative disorders and/or cancerous diseases and conditions, for
CC wound healing and epithelial cell proliferation, to treat inflammation or
CC infection, for treating thrombosis and arteriosclerosis, for treating or
CC preventing neural damage which occurs in neuronal disorders or
CC neurodegenerative conditions such as Alzheimer's disease and Parkinson's
CC disease, to enhance bone and periodontal regeneration and aid in tissue
CC transplants or bone grafts, to prevent skin aging or hair loss, to
CC stimulate growth and differentiation of haematopoietic cells and bone
CC marrow cells when used in combination with other cytokines, to maintain
CC organs before transplantation or for supporting cell culture of primary
CC tissues, to increase or decrease differentiation or proliferation of
CC embryonic stem cells, or to modulate mammalian characteristics or
CC metabolism. Note: The sequence data for this patent was published in
CC electronic format and is available from MIPD at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX
SQ Sequence 174 AA;
XX
XX
Query Match 24.5%; Score 128; DB 6; Length 174;
Best Local Similarity 100.0%; Pred. No. 3,5e-119;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
QY 395 LYRKHILQRKSPGRFVWLPLPSTHTIPYXPNLHPRPPSSRLPGITIGGYDQRP 454
LYRKHILQRKSPGRFVWLPLPSTHTIPYXPNLHPRPPSSRLPGITIGGYDQRP 454
Db 47 LYRKHILQRKSPGRFVWLPLPSTHTIPYXPNLHPRPPSSRLPGITIGGYDQRP 106
LYRKHILQRKSPGRFVWLPLPSTHTIPYXPNLHPRPPSSRLPGITIGGYDQRP 106
XX
XX
QY 455 PYVGDPISSLIPGGETPSPFPPLRPRFDPVGPLPGNPILPGRGPNDRFPPRSGRP 514
PYVGDPISSLIPGGETPSPFPPLRPRFDPVGPLPGNPILPGRGPNDRFPPRSGRP 514
XX
XX

Db 107 PYVGDPISSLIPGGETPSPFPPLRPRFDPVGPLPGNPILPGRGPNDRFPPRSGRP 166
QY 515 TDGRLSEFM 522
Db 167 TDGRLSEFM 174
XX
XX
RESULT 21
ADC74597
ID ADC74597 standard; protein; 174 AA.
XX
XX
AC ADC74597;
XX
XX
DT 01-JAN-2004 (first entry)
XX
XX
DE Human secreted protein - SEQ ID 1230.
XX
XX
XX
KW antihaemic; antithaemic; antiarrhythmic; antiinflammatory; antithyroid;
KW antidiabetic; immunosuppressive; dermatological; nephrotoxic;
KW antiparkinsonian; neuroprotective; nootropic; antibacterial; virucide;
KW fungicide; antiparasitic; antiarteriosclerotic; vulnerary; cyostatic;
KW haemopoietic; haematologic; anaemia; autoimmune disorder;
KW rheumatoid arthritis; inflammation; Grave's disease; diabetes;
KW systemic lupus erythematosus; glomerulonephritis; neurodegenerative;
KW Parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis;
KW cancer; bacterial; viral; fungal; parasitic infection; gene therapy;
KW human.
XX
XX
OS Homo sapiens.
XX
XX
PN WO2003038063-A2.
XX
XX
PD 08-MAY-2003.
XX
XX
PF 19-MAR-2002; 2002MO-US008277.
XX
XX
PR 21-MAR-2001; 2001US-0277340P.
XX
PR 19-JUL-2001; 2001US-0306171P.
XX
PR 13-NOV-2001; 2001US-0331287P.
XX
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX
PI Rosen CA, Ruben SM;
XX
XX
DR WPI; 2003-430516/40.
XX
XX
PT N-PSDB; ADC73982.
XX
XX
PT New human secreted polypeptide for diagnosing, preventing or treating
PT haematopoietic or hematologic disorders (e.g. anemia), autoimmune
PT disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer or
PT atherosclerosis).
XX
XX
PS Claim 16; SEQ ID NO 1230; 2272bp; English.
XX
XX
CC The invention relates to a novel human secreted polypeptide comprising a
CC defined sequence given in the specification. The polypeptide, nucleic
CC acid molecule, antibody, agonist or antagonist of the invention may be
CC useful for preparing a composition for diagnosing or treating a
CC haemopoietic or haematologic disorder such as anaemia, autoimmune
CC disorders such as rheumatoid arthritis, inflammation, Grave's disease,
CC diabetes, systemic lupus erythematosus or glomerulonephritis,
CC neurodegenerative disorders including Parkinson's disease and Alzheimer's
CC disease, wounds and hyperproliferative disorders including
CC atherosclerosis or cancer, as well as bacterial, viral, fungal or
CC parasitic infections. The polypeptide may also be used during gene
CC therapy procedures and for identifying a binding partner by contacting
CC the polypeptide with a binding partner and determining whether the
CC binding partner increases or decreases the activity of the polypeptide.
CC The current sequence is that of the human secreted protein of the
XX
XX
SQ Sequence 174 AA;
XX
XX

Query Match 24.5%; Score 128; DB 7; Length 174;
 Best Local Similarity 100.0%; Pred. No. 3.5e-119; Mismatches 0; Indels 0; Gaps 0;
 Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 395 LYKRHIORKESPCKGRFVMLPSSSTHTIPFYENPLHPRPFSSRLPGIIGEXYDQPTL 454
 DB 47 LYKRHIORKESPCKGRFVMLPSSSTHTIPFYENPLHPRPFSSRLPGIIGEXYDQPTL 106

QY 455 PYVGDPISLLIPGGETPSQFPPLRPDPVGPLPGPNPLPGRGGPNDRPFRPSGRP 514
 DB 107 PYVGDPISLLIPGGETPSQFPPLRPDPVGPLPGPNPLPGRGGPNDRPFRPSGRP 166

QY 515 TDGRLSFM 522
 DB 167 TDGRLSFM 174

RESULT 22
 AAY41397
 ID AAY41397 standard; protein; 175 AA.
 AC AAY41397;
 DT 02-DEC-1999 (first entry)
 DE Human secreted protein encoded by gene 90 clone HUSXS50.
 XX
 KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukemia;
 KW developmental abnormality; foetal deficiency; blood; allergy; renal;
 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
 KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
 XX
 OS Homo sapiens.
 PN WO9947540-A1.
 PD 23-SEP-1999.
 XX
 PF 18-MAR-1999; 99WO-US005804.
 XX
 PR 19-MAR-1998; 98US-0078563P.
 PR 19-MAR-1998; 98US-0078566P.
 PR 19-MAR-1998; 98US-0078573P.
 PR 19-MAR-1998; 98US-0078574P.
 PR 19-MAR-1998; 98US-0078576P.
 PR 19-MAR-1998; 98US-0078577P.
 PR 19-MAR-1998; 98US-0078578P.
 PR 19-MAR-1998; 98US-0078579P.
 PR 19-MAR-1998; 98US-0078581P.
 PR 01-APR-1998; 98US-0080312P.
 PR 01-APR-1998; 98US-0080313P.
 PR 01-APR-1998; 98US-0080314P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Ni J, Rosen CA, Yu G, Young PE, Fang P, Soppet DR;
 PI Wei Y, Andrews GA, Duan RD, Kyaw H, Ebner R, Lafleur DW, Olsen HS;
 PI Shi Y, Moore PA;
 XX
 DR WPI: 1999-562050/47.
 DR N-PSDB; AAZ24900.
 XX
 PT New isolated human genes, useful for diagnosis and treatment of e.g.
 PT cancers, neurological disorders, immune diseases, inflammation or blood
 PT disorders.
 XX
 PS Claim 11; Page 411; 484pp; English.
 XX

CC This sequence represents a secreted human protein encoded by the gene
 CC clone detailed in the descriptor line. The gene can be used to generate
 CC fusion proteins by linking to the gene to a human immunoglobulin Fc
 CC portion (e.g. AAZ24802) for increasing the stability of the fused protein
 CC as compared to the human protein only. The invention relates to 95 novel
 CC genes and their fragments (nucleic acid sequences: AAZ24811-24907; amino
 CC acid sequences AAY41308-Y41404) which are useful for preventing, treating
 CC or ameliorating medical conditions e.g. by protein or gene therapy. Also,
 CC pathological conditions can be diagnosed by determining the amount of the
 CC new polypeptides in a sample or by determining the presence of mutations
 CC in the new polynucleotides. Specific uses are described for each of the
 CC 95 polynucleotides, based on which tissues they are most highly expressed
 CC in (see AAZ24811 for described uses)
 CC
 SQ Sequence 175 AA;

Query Match 24.5%; Score 128; DB 2; Length 175;
 Best Local Similarity 100.0%; Pred. No. 3.5e-119; Mismatches 0; Indels 0; Gaps 0;
 Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 395 LYKRHIORKESPCKGRFVMLPSSSTHTIPFYENPLHPRPFSSRLPGIIGEXYDQPTL 454
 DB 47 LYKRHIORKESPCKGRFVMLPSSSTHTIPFYENPLHPRPFSSRLPGIIGEXYDQPTL 106

QY 455 PYVGDPISLLIPGGETPSQFPPLRPDPVGPLPGPNPLPGRGGPNDRPFRPSGRP 514
 DB 107 PYVGDPISLLIPGGETPSQFPPLRPDPVGPLPGPNPLPGRGGPNDRPFRPSGRP 166

QY 515 TDGRLSFM 522
 DB 167 TDGRLSFM 174

RESULT 23
 AAY83047
 ID AAY83047 standard; protein; 482 AA.
 XX
 AC AAY83047;
 DT 16-AUG-2000 (first entry)
 DE F-box protein FBP-7.
 XX
 KW F-box protein; FBP; diagnosis; treatment; screening; agonist; antagonist;
 KW proliferative disorder; differentiative disorder; breast cancer;
 KW prostate cancer; ovarian cancer; cancer; small cell lung carcinoma;
 KW immune disorder; cardiovascular disorder; inflammatory disorder; human.
 XX
 OS Homo sapiens.
 PN WO200012679-A1.
 PD 09-MAR-2000.
 XX
 PF 27-AUG-1999; 99WO-US019560.
 XX
 PR 28-AUG-1998; 98US-0098355P.
 PR 03-FEB-1999; 99US-0118568P.
 PR 15-MAR-1999; 99US-0124449P.
 XX
 PA (UYNY) UNIV NEW YORK STATE.
 XX
 PI Chiaur DS, Pagano M, Latres E;
 PI
 XX
 DR WPI: 2000-256635/22.
 DR N-PSDB; AAZ93356.
 XX
 PT Novel nucleic acid for screening compounds useful for treating
 PT proliferative and differentiative disorders such as cancer and immune
 PT disorders comprises sequences encoding ubiquitin ligases.
 XX
 PS Claim 10; Fig 10a; 245pp; English.
 XX

CC Nucleic acids encoding substrate-targeting subunits of ubiquitin ligases
CC with F-box motifs (F-box proteins) are useful for diagnosis of
CC proliferative and differentiated related disorders by measuring FBP gene
CC expression. Cells expressing such proteins or their fragments are useful
CC for screening compounds. The compounds are agonists or antagonists, which
CC are useful for treating a proliferative or differentiative disorder in a
CC mammal such as breast, ovarian and prostate cancer and small cell lung
CC carcinoma and also major opportunistic infections, immune disorders,
CC cardiovascular diseases and inflammatory disorders. FBP protein, analogs,
CC derivatives and their subsequences, anti-FBP antibodies are also useful
CC in diagnosis of the disorders

XX SQ Sequence 482 AA;

Query Match 16.5%; Score 86; DB 3; Length 482;
Best Local Similarity 100.0%; Pred. No. 9.4e-77;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 LCEGSSATLTCVPLGNLIVNATLKINNEISVKRLQLPSPFCKEKLGENVANIYKDL 301
DB 202 LCEGSSATLTCVPLGNLIVNATLKINNEISVKRLQLPSPFCKEKLGENVANIYKDL 261

QY 302 QKLSRLFKDQVLYPLAFTROALNLP 327
DB 262 QKLSRLFKDQVLYPLAFTROALNLP 287

RESULT 24

AAO22452
ID AAO22452 standard; protein; 482 AA.

AC AAO22452;

DT 11-OCT-2002 (first entry)

DE Human F-box protein FBP7 SEQ ID No 14.

XX Cytostratic; immunomodulator; cardiac; antiinflammatory; antitubercial;
XX proliferative; differentiative disorder; Skp2; F-box protein; cancer;
XX ubiquitin ligase; breast cancer; prostate cancer; ovarian cancer;
XX small cell lung carcinoma; immune disorder; parathyroid adenoma; FBP;
XX inflammatory disorder; lymphoma; major opportunistic infection;
XX certain cardiovascular disease; human.

XX Homo sapiens.

XX WO200255665-A2.

XX 18-JUL-2002.

XX 07-JAN-2002; 2002WO-US000311.

XX 05-JAN-2001; 2001US-0260179P.

XX (UNYNY) UNIV NEW YORK STATE.

XX Pagano M;

XX WPI: 2002-599665/64.

XX N-PSDB; AAL41047.

XX Screening compounds for treating proliferative disorders, e.g. breast
XX cancer or prostate cancer, infections or immune disorders, comprises
XX detecting a change in the activity of Skp2 with either p27 or Cks1.

XX Disclosure; Fig 10; 246pp; English.

XX The invention relates to screening compounds useful for the treatment of
XX proliferative or differentiative disorders comprising detecting a change
XX in the activity of Skp2 (F-box protein). The method is useful for
XX screening compounds for the treatment of proliferative or differentiative
XX disorders, particularly cancer. These compounds include small molecules,
XX or compounds or derivatives or analogues of the new ubiquitin ligases.

CC The compounds are useful for treating diseases such as cancer (e.g.
CC breast cancer, prostate cancer or ovarian cancer, lymphoma, small cell
CC lung carcinoma or parathyroid adenoma), major opportunistic infections,
CC immune disorders, certain cardiovascular diseases or inflammatory
CC disorders. This sequence represents an F-box protein (FBP) relating to
CC the invention

XX SQ Sequence 482 AA;

Query Match 16.5%; Score 86; DB 5; Length 482;
Best Local Similarity 100.0%; Pred. No. 9.4e-77;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 LCEGSSATLTCVPLGNLIVNATLKINNEISVKRLQLPSPFCKEKLGENVANIYKDL 301
DB 202 LCEGSSATLTCVPLGNLIVNATLKINNEISVKRLQLPSPFCKEKLGENVANIYKDL 261

QY 302 QKLSRLFKDQVLYPLAFTROALNLP 327
DB 262 QKLSRLFKDQVLYPLAFTROALNLP 287

RESULT 25

ABO54274
ID ABO54274 standard; protein; 76 AA.

AC ABO54274;

DT 29-JUL-2004 (first entry)

DE Human genome derived single exon protein #508.

XX Human; gene expression; single exon probe; microarray;
XX alternative splicing event; genomic alteration.

XX Homo sapiens.

XX US2003194704-A1.

XX 16-OCT-2003.

XX 03-APR-2002; 2002US-00029386.

XX 03-APR-2002; 2002US-00029386.

XX (PENK/) PENN S G.

XX (RANK/) RANK D R.

XX (HANK/) HANZEL D K.

XX Penn SG, Rank DR, Hanzel DK;

XX WPI: 2004-119264/12.

XX The invention relates to a nucleic acid probe for measuring human gene
XX expression, comprising any of the 27,400 fully defined nucleotide
XX sequences in the specification, or their complements or fragments, and
XX encoding at least 8 amino acids of any of the 688 amino acid sequences
XX fully defined in the specification. The probe is a single exon probe that
XX hybridises under high stringency conditions to a nucleic acid molecule
XX expressed in human cells or tissues. Also included are a spatially-
XX addressable set of single exon nucleic acid probes for measuring human
XX gene expression (comprising a plurality of single exon nucleic acid
XX probes cited above, where each of the plurality of probes is separately
XX and addressably isolatable or amplifiable from the plurality), a single
XX exon microarray for measuring human gene expression, a method of
XX measuring human gene expression, a vector comprising the single exon

CC probe cited above, an ORF-encoded peptide comprising at least 8
 CC contiguous amino acids of any of the above-mentioned amino acid
 CC sequences (optionally with conservative amino acid substitutions), an
 CC isolated antibody that binds specifically to a peptide cited above,
 CC methods of selling and/or licensing single exon probes or microarrays to
 CC a customer desiring to measure gene expression, a method of providing
 CC human gene expression data by subsequence, and a computer-readable
 CC storage medium which contains a database having a plurality of records
 CC (each record including data on the expression of a single exon probe
 CC cited above. The probe, methods and apparatus are useful in gene
 CC expression analysis. The probes may be used as tools for surveying
 CC tissues to detect the presence of expressed messages that contain their
 CC specific exon, or in constructing genome-derived single exon microarrays.
 CC In addition, the probes are used in identifying and characterizing
 CC alternative splicing events, in detecting and characterizing gross
 CC alterations in the genomic locus that includes their exon, in assessing
 CC smaller genomic alterations, in priming the synthesis of nucleic acids,
 CC or in expressing the ORF-encoded peptide. The present sequence is a human
 CC single exon probe protein of the invention. Note: The sequence data for
 CC this patent did not form part of the invention. Note: The sequence data for
 CC obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?docid=20030194704
 CC
 XX Sequence 76 AA;
 SQ
 Query Match 14.6%; Score 76; DB 8; Length 76;
 Best Local Similarity 100.0%; Pred. No. 1.9e-67;
 Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 140 LGPSQNEFASISQDNAMHAGTGYPSPEPMLCSFVSQGVPHSLETLTGASDCSDANDAL 139
 DB 1 LGPSQNEFASISQDNAMHAGTGYPSPEPMLCSFVSQGVPHSLETLTGASDCSDANDAL 60
 QY 200 IVLHLMBSGYIPQ 215
 DB 61 IVLHLMBSGYIPQ 76
 RESULT 26
 AAU32107
 ID AAU32107 standard; protein; 94 AA.
 AC AAU32107;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Novel human secreted protein #2598.
 XX
 KW Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WC200179449-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 16-APR-2001; 2001MO-US008656.
 XX
 PR 18-APR-2000; 2000US-00552929.
 PR 26-JAN-2001; 2001US-00770160.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Dmanac RT;
 XX
 DR WPI; 2001-611725/70.
 XX
 PT Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy.
 XX
 PS Claim 20; Page 556; 765bp; English.

XX The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising the
 CC nucleic acids encoding the polypeptides and cells genetically engineered
 CC to express them are also useful for producing the proteins. The proteins
 CC are useful in genetic vaccination, testing and therapy, and can be used
 CC as nutritional supplements. They may be used to increase stem cell
 CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
 CC and/or nerve tissue growth or regeneration; immune suppression and/or
 CC stimulation; as anti-inflammatory agents; and in treatment of leukemias.
 CC AAU29510-AAU33304 represent the amino acid sequences of novel human
 CC secreted proteins of the invention
 CC
 XX Sequence 94 AA;
 SQ
 Query Match 12.1%; Score 63; DB 4; Length 94;
 Best Local Similarity 100.0%; Pred. No. 2.3e-54;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 425 YENPLHPRFPSSRLPPGIGGYDQRTLPYVGDPISSLIPGDETPSPPLRPRDP 484
 DB 11 YENPLHPRFPSSRLPPGIGGYDQRTLPYVGDPISSLIPGDETPSPPLRPRDP 70
 QY 485 VGP 487
 DB 71 VGP 73
 RESULT 27
 AA87356
 ID AA87356 standard; protein; 113 AA.
 AC AA87356;
 XX
 DT 11-MAY-2000 (first entry)
 XX
 DE Human signal peptide containing protein HSP-133 SEQ ID NO:133.
 XX
 KW Human; signal peptide-containing protein; HSP; diagnosis; cancer;
 KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
 KW antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic;
 KW antiaesthetic; gene therapy; cell proliferation; neurological disorder;
 KW reproductive disorder; developmental disorder; arteriosclerosis;
 KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
 KW asthma; chronic disease; infection; Alzheimer's disease; schizophrenia;
 KW Parkinson's disease; Huntington's diseases; ovulatory defect;
 KW muscular dystrophy.
 XX
 OS Homo sapiens.
 XX
 PN WC200000610-A2.
 XX
 PD 06-JAN-2000.
 XX
 PF 25-JUN-1999; 99WO-US014484.
 XX
 PR 26-JUN-1998; 98US-0090762P.
 PR 31-JUL-1998; 98US-0094983P.
 PR 01-OCT-1998; 98US-0102686P.
 PR 11-DEC-1998; 98US-0112129P.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KT, Baughn MR;
 PI Aketkhem IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
 PI Bandman O;

DR WPI: 2000-160673/14.
DR N-PSDB: AA298241.
XX
XX
PT New human signal peptide-containing proteins useful in treatment,
PT prevention and diagnosis of e.g. cancer, inflammation and cardiovascular
PT disease.

PS Claim 1, Page 251, 327pp; English.

XX AA298109 to AA298242 encode AAY87224 to AAY87357 which represent the
CC human signal peptide-containing proteins HSP-1 to HSP-134. HSPs have
CC anticancer, anti-inflammatory, antimicrobial, neurotropic, hepatotropic,
CC neuroprotective, cardiovascular and antitumour activities, and can be
CC used in gene therapy. HSPs can be used to treat or prevent disorders
CC associated with decreased activity or function of HSP. Antagonists of
CC HSP are used to treat or prevent disorders associated with increased
CC activity or function of HSP. Such diseases include cell proliferation
CC (including cancer), inflammation, cardiovascular, neurological,
CC reproductive or developmental disorders, (e.g. arteriosclerosis,
CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
CC asthma, Crohn's disease, microbial or other infections, congestive or
CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSP
CC nucleic acids can be used for the recombinant production of HSP, for
CC detecting HSP in standard hybridisation and amplification assays (for
CC diagnosis and monitoring), in gene therapy, as antisense, triplex-forming
CC or ribozyme therapeutics, for detecting related sequences or genetic
CC variations, and for chromosomal mapping. HSP are also used to raise
CC specific antibodies (Ab) and to screen for agonists and antagonists
CC (potential therapeutic agents). Ab are used to diagnose, or monitor, HSP
CC -related diseases (in usual immunoassays), as therapeutic antagonists, in
CC competitive drug screens, and for purification of HSP from natural
CC sources

XX Sequence 113 AA;

Query Match 11.3%; Score 59; DB 3; Length 113;
Best Local Similarity 100.0%; Pred. No. 2.7e-50;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 323 ALNPDVGVGLVLPLELKRIFRLIDVRSVLSAVCRDFTASNDPLMRFYLDR 381
DB 22 ALNPDVGVGLVLPLELKRIFRLIDVRSVLSAVCRDFTASNDPLMRFYLDR 80

RESULT 28

ABG06838
ID ABG06838 standard; protein; 225 AA.

AC ABG06838;

DT 13-FEB-2002 (first entry)

XX Novel human diagnostic protein #6829.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US008631.

PR 31-MAR-2000; 2000US-00540217.

PA 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI: 2001-639362/73.
DR N-PSDB: AA571025.

XX
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostic, forensic, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

PS Claim 20; SEQ ID NO 37197; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (II) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG0377 represent novel human diagnostic
CC patient did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 225 AA;

Query Match 10.2%; Score 53; DB 4; Length 225;
Best Local Similarity 100.0%; Pred. No. 5.1e-44;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 329 VGVGLVLPLELKRIFRLIDVRSVLSAVCRDFTASNDPLMRFYLDR 381
DB 3 VGVGLVLPLELKRIFRLIDVRSVLSAVCRDFTASNDPLMRFYLDR 55

RESULT 29

ABO59862
ID ABO59862 standard; protein; 47 AA.

AC ABO59862;

DT 29-JUL-2004 (first entry)

XX Human genome derived single exon protein #6096.

KW Human; gene expression; single exon probe; microarray;
KW alternative splicing event; genomic alteration.

OS Homo sapiens.

PN US2003194704-A1.

PD 16-OCT-2003.

PF 03-APR-2002; 2002US-00029386.

PR 03-APR-2002; 2002US-00029386.

PA (PENN/) PENN S G.

PA (RANK/) RANK D R.

PA (HANZ/) HANZEL D K.

XX Penn SG, Rank DR, Hanzel DK;

DR WPI: 2004-119264/12.

XX New human genome-derived single exon nucleic acid probes useful for human
 PT gene expression analysis, for identifying or characterizing alternative
 PT splicing events, for assessing genomic alterations or as tools for
 PT surveying tissues.
 XX
 PS Claim 45; SEQ ID NO 33496; 80bp; English.
 CC The invention relates to a nucleic acid probe for measuring human gene
 CC expression, comprising any of the 27,400 fully defined nucleotide
 CC sequences in the specification, or their complements or fragments, and
 CC encoding at least 8 amino acids of any of the 6888 amino acid sequences
 CC fully defined in the specification. The probe is a single exon probe that
 CC hybridizes under high stringency conditions to a nucleic acid molecule
 CC expressed in human cells or tissues. Also included are a spatially-
 CC addressable set of single exon nucleic acid probes for measuring human
 CC gene expression (comprising a plurality of single exon nucleic acid
 CC probes cited above, where each of the plurality of probes is separately
 CC and addressably isolatable or amplifiable from the plurality), a single
 CC exon microarray for measuring human gene expression, a method of
 CC measuring human gene expression, a vector comprising the single exon
 CC probe cited above, an ORF-encoded peptide comprising at least 8
 CC contiguous amino acids of any of the above-mentioned amino acid
 CC sequences (optionally with conservative amino acid substitutions), an
 CC isolated antibody that binds specifically to a peptide cited above,
 CC a method of selling and/or licensing single exon probes or microarrays to
 CC a customer desiring to measure gene expression, a method of providing
 CC human gene expression data by subscription, and a computer-readable
 CC storage medium which contains a database having a plurality of records
 CC (each record including data on the expression of a single exon probe
 CC cited above). The probe, methods and apparatus are useful in gene
 CC expression analysis. The probes may be used as tools for surveying
 CC tissues to detect the presence of expressed messages that contain their
 CC specific exon, or in constructing genome-derived single exon microarrays.
 CC In addition, the probes are used in identifying and characterizing
 CC alternative splicing events, in detecting and characterizing gross
 CC alterations in the genomic locus that includes their exon, in assessing
 CC smaller genomic alterations, in priming the synthesis of nucleic acids,
 CC or in expressing the ORF-encoded peptide. The present sequence is a human
 CC single exon probe protein of the invention. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=20030194704
 CC
 XX
 SQ Sequence 47 AA:
 Query Match 9.0%; Score 47; DB 8; Length 47;
 Best Local Similarity 100.0%; Pred. No. 1.3e-38;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 216 GTEAKALSMPEKWLGSVYKLTQYHPLCEGSSATLTCVPLGNILVVA 262
 DB 1 GTEAKALSMPEKWLGSVYKLTQYHPLCEGSSATLTCVPLGNILVVA 47
 RESULT 30
 AAY83054
 ID AAY83054 standard; peptide; 39 AA.
 XX
 AC AAY83054;
 XX
 DT 16-AUG-2000 (first entry)
 DE F-box motif of FBP-6.
 XX
 XX F-box protein; FBP; diagnosis; treatment; screening; agonist; antagonist;
 KM proliferative disorder; differentiative disorder; breast cancer;
 KM prostate cancer; ovarian cancer; cancer; small cell lung carcinoma;
 KM immune disorder; cardiovascular disorder; inflammatory disorder; human.
 OS Homo sapiens.
 XX
 OS
 PN WO200012679-A1.

XX
 PD 09-MAR-2000.
 XX
 PF 27-AUG-1999; 99MO-US019560.
 XX
 XX 28-AUG-1998; 98US-0098355P.
 PR 03-FEB-1999; 99US-0118568P.
 PR 15-MAR-1999; 99US-0124449P.
 XX
 PA (UNYV) UNIV NEW YORK STATE.
 PI Chiari DS, Pagano M, Latres E;
 XX WPI, 2000-256635/22.
 DR
 XX Novel nucleic acid for screening compounds useful for treating
 PT proliferative and differentiative disorders such as cancer and immune
 PT disorders comprises sequences encoding ubiquitin ligases.
 XX
 PS Disclosure, Page 197; 245pp; English.
 CC Nucleic acids encoding substrate-targeting subunits of ubiquitin ligases
 CC with F-box motifs (F-box proteins) are useful for diagnosis of
 CC proliferative and differentiated related disorders by measuring FBP gene
 CC expression. Cells expressing such proteins or their fragments are useful
 CC for screening compounds. The compounds are agonists or antagonists, which
 CC are useful for treating a proliferative or differentiative disorder in a
 CC mammal such as breast, ovarian and prostate cancer and small cell lung
 CC carcinoma and also major opportunistic infections, immune disorders,
 CC cardiovascular diseases and inflammatory disorders. FBP protein, analogs,
 CC derivatives and their subsequences, anti-FBP antibodies are also useful
 CC in diagnosis of the disorders
 CC
 XX
 SQ Sequence 39 AA:
 Query Match 7.5%; Score 39; DB 3; Length 39;
 Best Local Similarity 100.0%; Pred. No. 1.1e-30;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 335 LPELKRIFRLDVRSTLSAVNCRDFTASNDPLWR 373
 DB 1 LPELKRIFRLDVRSTLSAVNCRDFTASNDPLWR 39
 RESULT 31
 AAO22459
 ID AAO22459 standard; peptide; 39 AA.
 XX
 AC AAO22459;
 XX
 DT 11-OCT-2002 (first entry)
 DE Human F-box motif amino residues of FBP SEQ ID NO 21.
 XX
 XX Cytostatic; immunomodulator; cardiac; antiinflammatory; antimicrobial;
 KM proliferative; differentiative disorder; Sg2; F-box protein; cancer;
 KM ubiquitin ligase; breast cancer; prostate cancer; ovarian cancer;
 KM small cell lung carcinoma; immune disorder; parathyroid adenoma; FBP;
 KM inflammatory disorder; lymphoma; major opportunistic infection;
 XX certain cardiovascular disease; human.
 XX
 OS Homo sapiens.
 XX
 PN WO200255665-A2.
 XX
 PD 18-JUL-2002.
 XX
 PD 07-JAN-2002; 2002MO-US000311.
 PF 05-JAN-2001; 2001US-0260179P.
 PR
 XX
 PA (UNYV) UNIV NEW YORK STATE.

PI Pagano M;
 XX
 DR MPI; 2002-595665/64.
 XX
 PT Screening compounds for treating proliferative disorders, e.g. breast
 PT cancer or prostate cancer; infections or immune disorders, comprises
 PT detecting a change in the activity of Skp2 with either p27 or Cks1.
 XX
 XX Disclosure; Fig 1; 246pp; English.
 XX
 CC The invention relates to screening compounds useful for the treatment of
 CC proliferative or differentiative disorders comprising detecting a change
 CC in the activity of Skp2 (F-box protein). The method is useful for
 CC screening compounds for the treatment of proliferative or differentiative
 CC disorders, particularly cancer. These compounds include small molecules,
 CC or compounds or derivatives or analogues of the new ubiquitin ligases.
 CC The compounds are useful for treating diseases such as cancer (e.g.
 CC breast cancer, prostate cancer or ovarian cancer, lymphoma, small cell
 CC lung carcinoma or parathyroid adenomas), major opportunistic infections,
 CC immune disorders, certain cardiovascular diseases or inflammatory
 CC disorders. This sequence represents a peptide of an F-box protein (FBP)
 CC relating to the invention
 CC
 CC Sequence 39 AA;
 XX
 SO
 Query Match 7.5%; Score 39; DB 5; Length 39;
 Best Local Similarity 100.0%; Pred. No. 1.1e-30;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 335 LPLEIKRIFRLLDVRVSLSSAVCRDLFTASNDPLMR 373
 DB 1 LPLEIKRIFRLLDVRVSLSSAVCRDLFTASNDPLMR 39
 RESULT 32
 AA02272
 ID AA02272 standard; protein, 38 AA.
 XX
 AC AA02272;
 XX
 DT 08-JUL-1999 (first entry)
 XX
 DE A F-box protein sequence.
 XX
 KM F-box protein; targeted ubiquitination; cellular protein;
 KM cell cycle regulator; transcription regulator; DNA replication;
 KM inflammatory response; infectious disease; protein degradation; cancer;
 KM virus infection.
 XX
 OS Homo sapiens.
 XX
 PN W0918989-A1.
 XX
 PD 22-APR-1999.
 XX
 PF 15-OCT-1998; 98MO-US021763.
 XX
 PR 16-OCT-1997; 97US-00951621.
 XX
 PA (BAYU) BAYLOR COLLEGE MEDICINE.
 XX
 PI Harper JW, Elledge SJ;
 XX
 DR MPI; 1999-277441/23.
 DR N-PSDB; AAX35546.
 XX
 PT New isolated F-box proteins and genes for development of therapeutics,
 PT e.g. for cancer treatment.
 XX
 PS Claim 3; Page 110; 170pp; English.
 CC AAX3553-51 encode F-box proteins (AA02249-77) which are involved in the
 CC targeted ubiquitination of cellular proteins. The F-box proteins are

CC involved in targeted ubiquitination of cellular proteins, including cell
 CC cycle regulators. The products and methods can be used for determining
 CC the interaction of these proteins with other proteins, e.g. to identify
 CC and/or investigate cell cycle regulators, transcription regulators,
 CC proteins involved in DNA replication, and other cellular regulatory
 CC proteins. They can be used in elucidating inflammatory response and
 CC infectious disease processes involving protein degradation as well as
 CC development of compounds that control (i.e. either enhance or retard)
 CC protein degradation, as appropriate to ameliorate the effects of the
 CC inflammatory response or disease process. They can be used for
 CC identifying and developing compounds effective against cancers or virus
 CC infection, e.g. immunodeficiency viruses such as HIV, feline
 CC immunodeficiency virus, bovine immunodeficiency virus, and simian
 CC immunodeficiency virus
 XX
 SO
 Sequence 38 AA;
 XX
 Query Match 7.3%; Score 38; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 1.1e-29;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 335 LPLEIKRIFRLLDVRVSLSSAVCRDLFTASNDPLM 372
 DB 1 LPLEIKRIFRLLDVRVSLSSAVCRDLFTASNDPLM 38
 RESULT 33
 AA08044
 ID AA08044 standard; peptide; 38 AA.
 XX
 AC AA08044;
 XX
 DT 01-NOV-2001 (first entry)
 XX
 DE Human F-box protein, F18 Phi.
 XX
 KM Human; nuclear factor-kappaB; NF-kB; regulatory factor; slimb protein;
 KM targeted ubiquitination; F-box protein; F18 Phi.
 XX
 OS Homo sapiens.
 XX
 PN US6232081-B1.
 XX
 PD 15-MAY-2001.
 XX
 PF 15-OCT-1998; 98US-00172841.
 XX
 PR 16-OCT-1997; 97US-00951621.
 XX
 PA (BAYU) BAYLOR COLLEGE MEDICINE.
 XX
 PI Harper JW, Elledge SJ, Winston JT;
 XX
 DR MPI; 2001-342771/36.
 DR N-PSDB; AAD14881.
 XX
 PT Detecting nuclear factor-kappaB regulatory factors, such as F-box
 PT proteins involved in targeted ubiquitination, by contacting the
 PT regulatory factors with slimb protein to form a complex and detecting the
 PT complex.
 XX
 PS Example 6; Fig 7; 69pp; English.
 XX
 CC The present invention relates to a method for detection of one or more
 CC nuclear factor (NF)-kappaB (KB) regulatory factors. The method comprises
 CC exposing a slimb protein to a sample suspected of containing one or more
 CC NF-kB regulatory factors, so that the slimb protein binds to one or more
 CC NF-kB regulatory factors to form a slimb/regulatory factor complex and
 CC detecting the slimb/regulatory factor complex. The method is useful for
 CC detecting NF-kB regulatory factors such as F-box proteins, IKBs, IKKs and
 CC agonists, antagonists and cofactors that interact with these factors. F-
 CC box proteins are involved in targeted ubiquitination of cellular
 CC proteins. The present sequence is human F-box protein, F18 Phi

XX
SQ Sequence 38 AA;

Query Match 7.3%; Score 38; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.1e-29;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 LPLELKLRIFRLDVRSVLSAVCRDLFTASNDPLIM 372
1 LPLELKLRIFRLDVRSVLSAVCRDLFTASNDPLIM 38

RESULT 34
AAB39652
ID AAB39652 standard; peptide; 38 AA.

AC AAB39652;
XX
XX 18-DEC-2003 (first entry)
XX Human F-box protein, F18 (phl).
XX Human F-box domain; E3 complex; ubiquitination; cell cycle regulator;
XX inflammatory disease.
XX Homo sapiens.
XX US6573094-B1.
XX 03-JUN-2003.
XX 16-OCT-1997; 97US-00951621.
XX 16-OCT-1997; 97US-00951621.
XX (BAYU) BAYLOR COLLEGE MEDICINE.
XX
XX Harper JW, Ellledge SJ;
XX WPI; 2003-776006/73.
XX N-PSDB; AAD60321.
XX
XX New isolated nucleic acid segment encoding a protein with at least one
XX functionally active F-box domain, useful for identifying related genes,
XX and for developing compounds for treating infectious or inflammatory
XX disease.
XX Example 6; Col 57-58; Opg; English.

XX The invention relates to an isolated nucleic acid segment comprising or
XX consisting essentially of a nucleic acid sequence encoding a protein
XX comprising at least one functionally active F-box domain sequence. The
XX polypeptide encoded by the nucleic acid segment is part of an E3 complex
XX involved in ubiquitination of cell cycle regulators and may be useful in
XX investigating mechanisms of infectious and inflammatory diseases and in
XX developing therapeutic agents for treating such diseases. The invention
XX is useful for detecting related polynucleotides encoding F-box proteins
XX and in the determination of the function of proteins such as elongin C,
XX Skp1-related protein, elongin B and elongin A. The present sequence is
XX human F-box protein
XX

SQ Sequence 38 AA;

Query Match 7.3%; Score 38; DB 7; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.1e-29;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 LPLELKLRIFRLDVRSVLSAVCRDLFTASNDPLIM 372
1 LPLELKLRIFRLDVRSVLSAVCRDLFTASNDPLIM 38

RESULT 35

ABG18509
ID ABG18509 standard; protein; 53 AA.

AC ABG18509;
XX
XX 18-FEB-2002 (first entry)
XX
XX Novel human diagnostic protein #18500.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder.
XX

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US008631.

PR 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

DR N-PSDB; AAS82696.

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

PS Claim 20; SEQ ID NO 48668; 103bp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX sequences. (I) is useful as hybridisation probes, polymerase chain
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX and in recombinant production of (II). The polynucleotides are also used
XX in diagnostics as expressed sequence tags for identifying expressed
XX genes. (I) is useful in gene therapy techniques to restore normal
XX activity of (II) or to treat disease, states involving (II). (II) is
XX useful for generating antibodies against it, detecting or quantitating a
XX polypeptide in tissue, as molecular weight markers and as a food
XX supplement. (II) and its binding partners are useful in medical imaging
XX of sites expressing (II). (I) and (II) are useful for treating disorders
XX involving aberrant protein expression or biological activity. The
XX polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
XX amino acid sequences of the invention. Note: The sequence data for this
XX patent did not appear in the printed specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pat_sequences
XX

SQ Sequence 53 AA;

Query Match 6.1%; Score 32; DB 4; Length 53;
Best Local Similarity 100.0%; Pred. No. 1.5e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 491 PNPILPGRGENDRPPFRPSRGRPTDGLSFM 522
22 PNPILPGRGENDRPPFRPSRGRPTDGLSFM 53

RESULT 36

AU32108
ID AU32108 standard; protein; 53 AA.

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XX AC AAU32108;
XX XX
XX DT 18-DEC-2001 (first entry)
XX DE Novel human secreted protein #2599.
XX KM Human; vaccination; gene therapy; nutritional supplement;
XX KM stem cell proliferation; haematopoiesis; nerve tissue regeneration;
XX KM immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX OS Homo sapiens.
XX PN WO200179449-A2.
XX PD 25-OCT-2001.
XX PF 16-APR-2001; 2001WO-US008656.
XX PR 18-APR-2000; 2000US-00552929.
XX PR 26-JAN-2001; 2001US-00770160.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Drmanac RT;
XX DR WPI, 2001-611725/70.
XX PT Nucleic acids encoding a range of human polypeptides; useful in genetic
XX PT vaccination, testing and therapy.
XX PS Claim 20; Page 556; 765pp; English.
XX CC The invention relates to novel human secreted polypeptides. The
XX CC polypeptides and antibodies to the polypeptides are useful for
XX CC determining the presence of or predisposition to a disease associated
XX CC with altered levels of polypeptide. The polypeptides are also useful for
XX CC identifying agents (agonists and antagonists) that bind to them. Cells
XX CC expressing the proteins are useful for identifying a therapeutic agent
XX CC for use in treatment of a pathology related to aberrant expression or
XX CC physiological interactions of the polypeptide. Vectors comprising the
XX CC nucleic acids encoding the polypeptides and cells genetically engineered
XX CC to express them are also useful for producing the proteins. The proteins
XX CC are useful in genetic vaccination, testing and therapy, and can be used
XX CC as nutritional supplements. They may be used to increase stem cell
XX CC proliferation, to regulate haematopoiesis, and in bone, cartilage, tendon
XX CC and/or nerve tissue growth or regeneration. Immune suppression and/or
XX CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
XX CC AAU29510-AAU3304 represent the amino acid sequences of novel human
XX CC secreted proteins of the invention
XX SQ
SQ Sequence 53 AA;
Query Match 6.1%; Score 32; DB 4; Length 53;
Best Local Similarity 100.0%; Pred. No. 1.5e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 491 PNPILPGRGGRNDPRFPFRSGRPDGRLSFM 522
DB 22 PNPILPGRGGRNDPRFPFRSGRPDGRLSFM 53

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XX KM cell cycle regulator; transcription regulator; DNA replication;
XX KM inflammatory response; infectious disease; protein degradation; cancer;
XX KM virus infection.
XX OS Mus sp.
XX PN WO9918989-A1.
XX PD 22-APR-1999.
XX PF 15-OCT-1998; 98WO-US021763.
XX PR 16-OCT-1997; 97US-00951621.
XX PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX PI Harper JM, Ellledge SJ;
XX PT WPI, 1999-277441/23.
XX DR N-PSDB; AAX35547.
XX PT New isolated F-box proteins and genes for development of therapeutics,
XX PT e.g. for cancer treatment.
XX PS Claim 4; Page 110; 170pp; English.
XX CC AAX35523-51 encode F-box proteins (AAV02249-77) which are involved in the
XX CC targeted ubiquitination of cellular proteins. The F-box proteins are
XX CC involved in targeted ubiquitination of cellular proteins, including cell
XX CC cycle regulators. The products and methods can be used for determining
XX CC the interaction of these proteins with other proteins, e.g. to identify
XX CC and/or investigate cell cycle regulators, transcription regulators,
XX CC proteins involved in DNA replication, and other cellular regulatory
XX CC proteins. They can be used in elucidating inflammatory response and
XX CC infectious disease processes involving protein degradation as well as
XX CC development of compounds that control (i.e. either enhance or retard)
XX CC protein degradation, as appropriate to ameliorate the effects of the
XX CC inflammatory response or disease process. They can be used for
XX CC identifying and developing compounds effective against cancers or virus
XX CC infection, e.g. immunodeficiency viruses such as HIV, feline
XX CC immunodeficiency virus, bovine immunodeficiency virus, and simian
XX CC immunodeficiency virus
XX SQ
SQ Sequence 38 AA;
Query Match 2.9%; Score 15; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 335 LPLEKLRIRFLDV 349
DB 1 LPLEKLRIRFLDV 15

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RESULT 37
AAV02273
ID AAV02273 standard; protein; 38 AA.
XX
XX AAV02273;
XX
XX 08-JUN-1999 (first entry)
XX
XX A F-box protein sequence.
XX
XX F-box protein; targeted ubiquitination; cellular protein.

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RESULT 38
AAE08045
ID AAE08045 standard; peptide; 38 AA.
XX
XX AAE08045;
XX
XX 01-NOV-2001 (first entry)
XX
XX Mouse F-box protein, F18 phi.
XX
XX Mouse; nuclear factor-kappaB; NF-kB; regulatory factor; slimb protein;
XX KM targeted ubiquitination; F-box protein; F18 phi.
XX
XX Mus musculus.
XX
XX US6232081-B1.
XX
XX 15-MAY-2001.
XX

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PF 15-OCT-1998; 98US-00172841.
XX
PR 16-OCT-1997; 97US-00951621.
XX
PA (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI Harper JW, Ellledge SJ, Winston JT;
XX
DR WPI; 2001-342771/36.
DR N-PSDB; AAD14882.
XX
PT Detecting nuclear factor-kappaB regulatory factors, such as F-box
PT proteins involved in targeted ubiquitination, by contacting the
PT regulatory factors with slimb protein to form a complex and detecting the
PT complex.
XX
PS Example 6; Fig 7; 69pp; English.
XX
CC The present invention relates to a method for detection of one or more
CC nuclear factor (NF)-kappaB (KB) regulatory factors. The method comprises
CC exposing a slimb protein to a sample suspected of containing one or more
CC NF-kB regulatory factors, so that the slimb protein binds to one or more
CC NF-kB regulatory factors to form a slimb/regulatory factor complex and
CC detecting the slimb/regulatory factor complex. The method is useful for
CC detecting NF-kB regulatory factors such as F-box proteins, IKKs, IKKs and
CC agonists, antagonists and cofactors that interact with these factors. F-
CC box proteins are involved in targeted ubiquitination of cellular
CC proteins. The present sequence is mouse F-box protein, F18 Phi
XX
SQ Sequence 38 AA;
XX
Query Match 2.9%; Score 15; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 335 LPLEKLRIFRLDV 349
DB 1 LPLEKLRIFRLDV 15
XX
RESULT 39
AAB39653
ID AAB39653 standard; peptide; 38 AA.
XX
AC AAB39653;
XX
DT 18-DEC-2003 (first entry)
XX
DE Mouse F-box protein, F18 (phi).
XX
KM Mouse; F-Box domain; B3 complex; ubiquitination; cell cycle regulator;
KM inflammatory disease.
XX
OS Homo sapiens.
XX
PN US6573094-B1.
XX
PD 03-JUN-2003.
XX
PF 16-OCT-1997; 97US-00951621.
XX
PR 16-OCT-1997; 97US-00951621.
XX
PA (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI Harper JW, Ellledge SJ;
XX
DR WPI; 2003-776006/73.
DR N-PSDB; AAD60322.
XX
PT New isolated nucleic acid segment encoding a protein with at least one
PT functionally active F-box domain, useful for identifying related genes,
PT and for developing compounds for treating infectious or inflammatory

```

```

PT disease.
XX
PS Example 6; Col 57-58; Opp; English.
XX
CC The invention relates to an isolated nucleic acid segment comprising or
CC consisting essentially of a nucleic acid sequence encoding a protein
CC comprising at least one functionally active F-box domain sequence. The
CC polypeptide encoded by the nucleic acid segment is part of an E3 complex
CC involved in ubiquitination of cell cycle regulators and may be useful in
CC investigating mechanisms of infectious and inflammatory diseases and in
CC developing therapeutic agents for treating such diseases. The invention
CC is useful for detecting related polynucleotides encoding F-box proteins
CC and in the determination of the function of proteins such as elongin C,
CC Skp1-related protein, elongin B and elongin A. The present sequence is
CC mouse F-box protein
XX
SQ Sequence 38 AA;
XX
Query Match 2.9%; Score 15; DB 7; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 335 LPLEKLRIFRLDV 349
DB 1 LPLEKLRIFRLDV 15
XX
RESULT 40
AAY41578
ID AAY41578 standard; protein; 13 AA.
XX
AC AAY41578;
XX
DT 02-DEC-1999 (first entry)
XX
DE Fragment of human secreted protein encoded by gene 90.
XX
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS Homo sapiens.
XX
PN WO947540-A1.
XX
PD 23-SEP-1999.
XX
PF 18-MAR-1999; 99WO-US005804.
XX
PR 19-MAR-1998; 98US-0078563P.
PR 19-MAR-1998; 98US-0078566P.
PR 19-MAR-1998; 98US-0078573P.
PR 19-MAR-1998; 98US-0078574P.
PR 19-MAR-1998; 98US-0078576P.
PR 19-MAR-1998; 98US-0078577P.
PR 19-MAR-1998; 98US-0078578P.
PR 19-MAR-1998; 98US-0078579P.
PR 19-MAR-1998; 98US-0078581P.
PR 19-MAR-1998; 98US-0078581P.
PR 01-APR-1998; 98US-0080313P.
PR 01-APR-1998; 98US-0080313P.
PR 01-APR-1998; 98US-0080313P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Ni J, Rosen CA, Yu G, Young PE, Feng P, Soppet DR;
PI Wei Y, Endress GA, Duan RD, Kyaw H, Ebner R, Lafleur DW, Olsen HS;
PI Shi Y, Moore PA;
XX

```

DR WPI: 1999-562050/47.

XX
XX New isolated human genes, useful for diagnosis and treatment of e.g.
PT cancers, neurological disorders, immune diseases, inflammation or blood
PT disorders.

XX
XX Disclosure: Page 167; 484pp; English.

XX
XX This sequence represents a fragment of a secreted human protein encoded
CC by the nucleic acid molecule detailed in the descriptor line. The gene
CC can be used to generate fusion proteins by linking to the gene to a human
CC immunoglobulin Fc portion (e.g. AA224802) for increasing the stability of
CC the fused protein as compared to the human protein only. The invention
CC relates to 95 novel genes and their fragments (nucleic acid sequences:
CC AA224811-224907; amino acid sequences AA41308-Y41404) which are useful
CC for preventing, treating or ameliorating medical conditions e.g. by
CC protein or gene therapy. Also, pathological conditions can be diagnosed
CC by determining the amount of the new polypeptides in a sample or by
CC determining the presence of mutations in the new polynucleotides.
CC Specific uses are described for each of the 95 polynucleotides, based on
CC which tissues they are most highly expressed in (see AA224811 for
CC described uses)

XX
XX Sequence 13 AA;

SO Query Match 2.5%; Score 13; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 321 ROALNLPVFGIV 333
DB 1 ROALNLPVFGIV 13

RESULT 41
AA41577
ID AA41577 standard; protein; 13 AA.

XX
XX AA41577;
DT 02-DEC-1999 (first entry)

XX
XX Fragment of human secreted protein encoded by gene 90.

XX
XX Human; secreted protein; fusion protein; gene therapy; protein therapy;
KM diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KM developmental abnormality; foetal deficiency; blood; allergy; renal;
KM immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KM inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KM cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KM osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KM endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

XX
XX Homo sapiens.

XX
XX WO9947540-A1.
PN 23-SEP-1999.

XX
XX 18-MAR-1999; 99WO-US005804.

XX
XX 19-MAR-1998; 98US-0078563P.
XX 19-MAR-1998; 98US-0078566P.
XX 19-MAR-1998; 98US-0078573P.
XX 19-MAR-1998; 98US-0078574P.
XX 19-MAR-1998; 98US-0078576P.
XX 19-MAR-1998; 98US-0078577P.
XX 19-MAR-1998; 98US-0078578P.
XX 19-MAR-1998; 98US-0078579P.
XX 19-MAR-1998; 98US-0078581P.
XX 01-APR-1998; 98US-0080312P.
XX 01-APR-1998; 98US-0080313P.
XX 01-APR-1998; 98US-0080314P.

XX
XX (HUMA-) HUMAN GENOME SCI INC.

XX
XX Ruben SM, Ni J, Rosen CA, Yu G, Young PE, Feng P, Soppet DR;
PI Wei Y, Endress GA, Duan RD, Kyaw H, Ebner R, Lafleur DW, Olsen HS;
PI Shi Y, Moore PA;
XX
XX WPI: 1999-562050/47.

XX
XX New isolated human genes, useful for diagnosis and treatment of e.g.
PT cancers, neurological disorders, immune diseases, inflammation or blood
PT disorders.

XX
XX Disclosure: Page 167; 484pp; English.

XX
XX This sequence represents a fragment of a secreted human protein encoded
CC by the nucleic acid molecule detailed in the descriptor line. The gene
CC can be used to generate fusion proteins by linking to the gene to a human
CC immunoglobulin Fc portion (e.g. AA224802) for increasing the stability of
CC the fused protein as compared to the human protein only. The invention
CC relates to 95 novel genes and their fragments (nucleic acid sequences:
CC AA224811-224907; amino acid sequences AA41308-Y41404) which are useful
CC for preventing, treating or ameliorating medical conditions e.g. by
CC protein or gene therapy. Also, pathological conditions can be diagnosed
CC by determining the amount of the new polypeptides in a sample or by
CC determining the presence of mutations in the new polynucleotides.
CC Specific uses are described for each of the 95 polynucleotides, based on
CC which tissues they are most highly expressed in (see AA224811 for
CC described uses)

XX
XX Sequence 13 AA;

SO Query Match 2.5%; Score 13; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 308 FKDQVYPLAFT 320
DB 1 FKDQVYPLAFT 13

RESULT 42
AAM94240
ID AAM94240 standard; protein; 57 AA.

XX
XX AAM94240;
DT 21-NOV-2001 (first entry)

XX
XX Human reproductive system related antigen SEQ ID NO: 2898.

XX
XX Human; reproductive system related antigen; reproductive system disorder;
KM cancer; gene therapy.

XX
XX Homo sapiens.

XX
XX WO200155320-A2.
PN 02-AUG-2001.

XX
XX 17-JUN-2001; 2001WO-US001339.

XX
XX 31-JAN-2000; 2000US-0179065P.
XX 04-FEB-2000; 2000US-0180628P.
XX 24-FEB-2000; 2000US-0184664P.
XX 02-MAR-2000; 2000US-0186350P.
XX 16-MAR-2000; 2000US-0189874P.
XX 17-MAR-2000; 2000US-0190076P.
XX 18-APR-2000; 2000US-0198123P.
XX 19-MAY-2000; 2000US-020515P.
XX 07-JUN-2000; 2000US-0209467P.
XX 28-JUN-2000; 2000US-0214886P.
XX 30-JUN-2000; 2000US-0215135P.

Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 406 SPKGRFVM 413
Db 1 SPKGRFVM 8

RESULT 43

ABO55854
ID ABO55854 standard; protein; 63 AA.

XX ABO55854;

XX 29-JUN-2004 (first entry)

XX Human genome derived single exon protein #2088.

XX Human; gene expression; single exon probe; microarray;

XX alternative splicing event; genomic alteration.

XX Homo sapiens.

XX US2003194704-A1.

XX 16-OCT-2003.

XX 03-APR-2002; 2002US-00029386.

XX 03-APR-2002; 2002US-00029386.

XX (PENN/) PENN S G.

XX (RANK/) RANK D R.

XX (HANTZ/) HANTZEL D K.

XX Penn SG, Rank DR, Hanzel DK;

XX WPI; 2004-119264/12.

XX New human genome-derived single exon nucleic acid probes useful for human
XX gene expression analysis, for identifying or characterizing alternative
XX splicing events, for assessing genomic alterations or as tools for
XX surveying tissues.

XX Claim 45; SEQ ID NO 29488; 80bp; English.

XX The invention relates to a nucleic acid probe for measuring human gene
XX expression, comprising any of the 27,400 fully defined nucleotide
XX sequences in the specification, or their complements or fragments, and
XX encoding at least 8 amino acids of any of the 6888 amino acid sequences
XX fully defined in the specification. The probe is a single exon probe that
XX hybridizes under high stringency conditions to a nucleic acid molecule
XX expressed in human cells or tissues. Also included are a spatially-
XX addressable set of single exon nucleic acid probes for measuring human
XX gene expression (comprising a plurality of single exon nucleic acid
XX probes cited above, where each of the plurality of probes is separately
XX and addressably isolatable or amplifiable from the plurality), a single
XX exon microarray for measuring human gene expression, a method of
XX measuring human gene expression, a vector comprising the single exon
XX probe cited above, an ORF-encoded peptide comprising at least 8
XX contiguous amino acids of any of the above-mentioned amino acid
XX sequences (optionally with conservative amino acid substitutions), an
XX isolated antibody that binds specifically to a peptide cited above,
XX methods of selling and/or licensing single exon probes or microarrays to
XX a customer desiring to measure gene expression, a method of providing
XX human gene expression data by subscription, and a computer-readable
XX storage medium which contains a database having a plurality of records
XX (each record including data on the expression of a single exon probe
XX cited above). The probe, methods and apparatus are useful in gene
XX expression analysis. The probe may be used as tools for surveying
XX tissues to detect the presence of expressed messages that contain their
XX specific exon, or in constructing genome-derived single exon microarrays.
XX In addition, the probes are used in identifying and characterizing

CC alternative splicing events, in detecting and characterizing gross
CC alterations in the genomic locus that includes their exon, in assessing
CC smaller genomic alterations, in priming the synthesis of nucleic acids,
CC or in expressing the ORF-encoded peptide. The present sequence is a human
CC single exon probe protein of the invention. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030194704

XX Sequence 63 AA;

XX Query Match 1.5%; Score 8; DB 8; Length 63;

XX Best Local Similarity 100.0%; Pred. No. 18;

XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 350 RSVLSLSA 357
Db 32 RSVLSLSA 39

RESULT 44

ABP10900
ID ABP10900 standard; protein; 92 AA.

XX ABP10900;

XX 25-JUN-2002 (first entry)

XX Human ORFX protein sequence SEQ ID NO:21782.

XX Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;

XX hyperproliferative disorder; psoriasis; benign tumor; hemorrhage;

XX degenerative disorder; osteoarthritis; neurodegenerative disorder;

XX cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;

XX hypertension; hypothyroidism; cholesterol ester storage disease;

XX immune deficiency; immune disorder; infectious disease;

XX autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;

XX myasthenia gravis.

XX Homo sapiens.

XX WO200192523-A2.

XX 06-DEC-2001.

XX 29-MAY-2001; 2001WO-US010836.

XX 30-MAY-2000; 2000US-0206132P.

XX 29-AUG-2000; 2000US-0228716P.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach MD;

XX WPI; 2002-106308/14.

XX N-PSDB; ABN26652.

XX Novel human polypeptides and polynucleotides useful for diagnosing,

XX preventing and treating cardiovascular disease, neurodegenerative,

XX hyperproliferative disorders and autoimmune disorders.

XX The present invention describes substantially purified human proteins
XX (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
XX in the specification). ABN15762 to ABN27252 encode the human ORFX
XX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
XX treating or preventing a pathology associated with an ORFX-associated
XX disorder in humans, and in the manufacture of a medicament for treating a
XX syndrome associated with ORFX-associated disorder. ORFX polynucleotide
XX sequences can be used in gene therapy. ORFX sequences can be used in the
XX treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
XX psoriasis, benign tumors, keloid, degenerative disorders, hemorrhage,

osteoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious diseases, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORF proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or peridontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, CC reperfusion injury in various tissues and conditions resulting from CC systemic cytokine damage. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 92 AA;

Query Match 1.5%; Score 8; DB 5; Length 92;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 471 TPSEQPPL 478
|||
72 TPSEQPPL 79

RESULT 45
AAU55117
ID AAU55117 standard; protein; 183 AA.

AC AAU55117;

XX 27-FEB-2002 (first entry)

XX Propionibacterium acnes immunogenic protein #16013.

XX SAPHO syndrome; synovitis; acne; pustulosis; hyperostosis; osteomyelitis;
XX uveitis; endophthalmitis; bone; joint; central nervous system; ELISA,
XX inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
XX dermatological; osteopathic; neuroprotectant.

XX Propionibacterium acnes.

XX WO200181581-A2.

XX 01-NOV-2001.

XX 20-APR-2001; 2001WO-US012865.

XX 21-APR-2000; 2000US-0199047P.

XX 02-JUN-2000; 2000US-0208841P.

XX 07-JUL-2000; 2000US-0216747P.

XX (CORI-) CORIXA CORP.

XX Skeiky YAM, Persing DH, Mitcham JL, Wang SS, Bhatia A;

XX L'maisonneuve J, Zhang Y, Jen S, Carter D;

XX WPI: 2001-616774/71.

XX N-PSDB; AAS59568.

XX Propionibacterium acnes polypeptides and nucleic acids useful for

XX vaccinating against and diagnosing infections, especially useful for

XX treating acne vulgaris.

XX Example 1; SEQ ID NO 16312; 1069PD; English.

XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic

XX polypeptides. The proteins and their associated DNA sequences are used in

XX the treatment, prevention and diagnosis of medical conditions caused by

XX P. acnes. The disorders include SAPHO syndrome (synovitis, acne,

XX pustulosis, hyperostosis and osteomyelitis), uveitis and endophthalmitis.

XX P. acnes is also involved in infections of bone, joints and the central

nervous system, however it is particularly involved in the inflammatory

CC lesions associated with acne vulgaris. A method for detecting the

CC presence or absence of P. acnes in a patient comprises contacting a

CC sample with a binding agent that binds to the proteins of the invention

CC and determining the amount of bound protein in the sample. The

CC polypeptides may be used as antigens in the production of antibodies

CC specific for P. acnes proteins. These antibodies can be used to

CC downregulate expression and activity of P. acnes polypeptides and

CC therefore treat P. acnes infections. The antibodies may also be used as

CC diagnostic agents for determining P. acnes presence, for example, by

CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for

CC this patent did not form part of the printed specification, but was

CC obtained in electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 183 AA;

Query Match 1.5%; Score 8; DB 4; Length 183;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 VPETEPPL 23
|||
137 VPETEPPL 144

RESULT 46
ABMS1636
ID ABMS1636 standard; protein; 183 AA.

AC ABMS1636;

XX 20-OCT-2003 (first entry)

XX Propionibacterium acnes predicted ORF-encoded polypeptide #16312.

XX Acne vulgaris; antiseborrheic; dermatological; antibacterial;
XX immunostimulant; immune response; vaccine.

XX Propionibacterium acnes.

XX WO2003033515-A1.

XX 24-APR-2003.

XX 11-OCT-2002; 2002WO-US032727.

XX 15-OCT-2001; 2001US-00978825.

XX (CORI-) CORIXA CORP.

XX Mitcham JL, Skeiky YAM, Persing DH, Bhatia A, Maisonneuve JL;

XX Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;

XX Barth B, Vallieve-Douglass J;

XX WPI: 2003-381789/36.

XX N-PSDB; ACF64497.

XX New Propionibacterium acnes polypeptides and polynucleotides encoding the

XX polypeptide, useful for diagnosing, preventing or treating acne vulgaris,

XX or for stimulating an immune response specific for a P. acnes protein.

XX Example 1; SEQ ID NO 16312; 1481PD; English.

XX The invention relates to an isolated polynucleotide (ACF64435-ACF64733)

XX encoding a Propionibacterium acnes protein. The invention also relates to

XX polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to

XX immunogenic fragments of P. acnes polypeptides. The invention

XX additionally encompasses expression vectors and host cells comprising a

XX polynucleotide of the invention; antibodies against polypeptides of the

XX invention; fusion proteins comprising a polypeptide of the invention; a

XX method for stimulating an immune response specific for a P. acnes

XX polypeptide and an isolated T cell population comprising T cells prepared

via this method; a vaccine composition (comprising P. acnes polypeptides, CC polynucleotides, antibodies, fusion proteins, T cell populations, or CC antigen-presenting cells that express the polypeptide); a method and kit CC for detecting or determining the presence or absence of P. acnes in a CC patient; and a method for inhibiting the development of P. acnes in a CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion CC proteins, T cell populations or antigen-presenting cells that express the CC polypeptides are useful for diagnosing, preventing or treating acne CC vulgaris, or for stimulating an immune response specific for P. acnes CC protein. The polynucleotides can also be used as probes or primers for CC nucleic acid hybridisation. The vaccine composition is useful for the CC stimulation of an immune response against P. acnes, or for treating acne, CC and the kit is useful for performing a diagnostic assay. The present CC sequence represents a polypeptide predicted to be encoded by an ORF (open CC reading frame) contained within the P. acnes polynucleotides of the CC invention. Note: The sequence data for this patent did not form part of CC the printed specification, but was obtained in electronic format directly CC from WIPO at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences) CC XX

Sequence 183 AA;

Query Match 1.5%; Score 8; DB 6; Length 183;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 VPETEPPTL 23
|||
DB 137 VPETEPPTL 144

RESULT 47
AAG32036
ID AAG32036 standard; protein; 572 AA.

AC AAG32036;
XX
DI 17-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana protein fragment SEQ ID NO: 38575.
DE
XX Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
XX Arabidopsis thaliana.
OS
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
XX 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130448P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-01310891P.
PR 30-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 04-MAY-1999; 99US-0132407P.
PR 05-MAY-1999; 99US-0132484P.
PR 06-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.

PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-01334256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142877P.
PR 13-JUL-1999; 99US-0143342P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144684P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.


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PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145961P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149902P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0156589P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157533P.
PR 06-OCT-1999; 99US-0158029P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.

PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 26-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161924P.
PR 28-OCT-1999; 99US-0161932P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 1.5%; Score 8; DB 3; Length 572;
Best Local Similarity 100.0%; Pred.No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 DUCHILO 79
Db 96 DUCHILO 103

RESULT 48
AAG66450
ID AAG66450 standard; protein; 628 AA.
XX
AC AAG66450;
XX
DT 16-NOV-2001 (first entry)
XX
DE Murine beta-netrin.
XX
KM Murine; beta-netrin; cytostatic; Neurotrophic; Neuroprotective; Vasotropic;
KM vulnary; gene therapy; neurite growth; neurite guidance; renal cancer;
KM neurite stability; cell proliferation; angiogenesis; Alzheimer's;
KM muscular development; muscular innervation; tumour; ovarian cancer;
KM neurological disorder; cardiovascular disorder; ischaemia.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Misc-difference 31 /note= "Encoded by GAC"
FT Misc-difference 132.1134 /note= "Encoded by ATG GTG TTC"
FT Misc-difference 227 /note= "Encoded by ATG GTG TTC"
FT Misc-difference 227 /note= "Encoded by CCG"
FT Misc-difference 249 /note= "Encoded by ATG"
FT Misc-difference 341 /note= "Encoded by TCT"
FT Misc-difference 558 /note= "Encoded by AAC"
XX
PN WO200164837-A2.
XX
PD 07-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US006413.
XX
XX 29-FEB-2000; 2000US-0185811P.
PR 01-SEP-2000; 2000US-0229893P.
XX
PA (SEHO) GEN HOSPITAL CORP.
XX
XX Burgeson R, Brunken W, Koch M, Hunter D, Olson P;
PI WPI; 2001-550173/61.
XX DR N-PSDB; AAH75956.
XX
PT Novel beta-netrin polypeptides, polynucleotides useful in neurite
outgrowth, stability, modulating angiogenesis, cell proliferation and for
```

PT	treating and preventing cancer, neurological and cardiovascular disorders.
XX	
PS	Claim 5; Fig 3; 140pp; English.
CC	The present sequence is the protein sequence for murine beta-netrin. Beta-
CC	netrin is useful in neutre growth, guidance and/or stability. Beta-
CC	netrin is also useful in cell proliferation, development of the vascular
CC	system, angiogenesis, muscular development or innervation. Beta-netrin
CC	inhibits tumour growth and angiogenesis in tumours therefore, beta-netrin
CC	is useful in treating ovarian and renal cancer. Also, beta-netrin is
CC	useful for treating neurological (e.g. Alzheimer's) and cardiovascular
CC	disorders (e.g. ischaemia)
XX	
SQ	Sequence 628 AA;
Query Match	1.5%; Score 8; DB 4; Length 628;
Best Local Similarity	100.0%; Pred. No. 1.4e+02;
Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Qy	3 LRVRLTKR 10
Dd	224 LRVRLTKR 231
RESULT 49	
ID	ABU21326
XX	ABU21326 standard; protein; 789 AA.
AC	ABU21326;
XX	
DT	19-JUN-2003 (first entry)
XX	
DE	Protein encoded by Prokaryotic essential gene #6853.
XX	
KM	Antisense; prokaryotic essential gene; cell proliferation; drug design.
OS	Burkholderia fungorum.
XX	
PN	WO200277183-A2.
XX	
PD	03-OCT-2002.
PF	
XX	21-MAR-2002; 2002WO-US009107.
PR	21-MAR-2001; 2001US-00815242.
XX	
PR	06-SEP-2001; 2001US-00948993.
XX	
PR	25-OCT-2001; 2001US-0342923F.
XX	
PR	08-FEB-2002; 2002US-00072851.
XX	
PR	06-MAR-2002; 2002US-0362899F.
XX	
PA	(EIT-) ELITRA PHARM INC.
XX	
P1	Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KU, Zyskind JW,
XX	Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
DR	WPI: 2003-0299926/02.
N-PSDB; ACR25196.	
PT	New antisense nucleic acids, useful for identifying proteins or screening
PT	for homologous nucleic acids required for cellular proliferation to
PT	isolate candidate molecules for rational drug discovery programs.
XX	
PS	Claim 25; SEQ ID NO 49250; 1766pp; English.
XX	
CC	The invention relates to an isolated nucleic acid comprising any one of
CC	the 6213 antisense sequences given in the specification where expression
CC	of the nucleic acid inhibits proliferation of a cell. Also included are:
CC	(1) a vector comprising a promoter operably linked to the nucleic acid
CC	encoding a polypeptide whose expression is inhibited by the antisense
CC	nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC	polypeptide or its fragment whose expression is inhibited by the
CC	antisense nucleic acid; (4) an antibody capable of specifically binding

Cc		the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pat_sequences
Sq	Sequence 789 AA;	
Dy	Query Match Best Local Similarity 1.5%; Score 8; DB 6; Length 789; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0	324 LNLDPVFG 331 727 LNLDPVFG 734
ID	RESULT 50 ADCS4146 ADCS4146 standard; peptide; 13 AA.	
Ac	ADC54146;	
Xx	18-DEC-2003 (first entry)	
Dt	Pepptide linker #1.	
Xx	Pepptide linker.	
Km	Unidentified.	
Oz	JP2003159069-A.	
Fv	03-JUN-2003.	
Pd	21-NOV-2001; 2001JP-00356652.	
Xx	21-NOV-2001; 2001JP-00356652.	
Pr	(KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN. PA (KOZU-) KOKURITSU YODO EISEI KENKYUSHO. XX (XOXU-) KOKURITSU YODO EISEI KENKYUSHO. DR WPI; 2003-818676/77.	
Ps	Novel fusion selective marker gene comprising drug-resistance gene coupled to reporter gene, useful for manufacturing recombinant proteins.	
Ex	Example 1; Fig 1; 11pp; Japanese.	
Cc	The present invention relates to a fusion selective marker gene (I) comprising a drug-resistance gene (II) coupled to a reporter gene (III) by a base sequence encoding buffer amino acid sequence. (II) is a puvomycin N-acetyl transferase gene (pac) and (III) is an enhanced green fluorescent protein (EGFP). (I) is useful for manufacturing recombinant protein. (I) is also useful for identifying a desired protein. (I)	

CC enables manufacture of recombinant protein, and improved identification
 CC of expression of desired gene. The present sequence is a peptide linker
 CC which was used to illustrate the invention.

XX
 SQ Sequence 13 AA;

Query Match 1.3%; Score 7; DB 7; Length 13;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 337 LEIKLRI 343
 DB 4 LEIKLRI 10

RESULT 51
 AAR72285
 ID AAR72285 standard; peptide; 20 AA.

XX AAR72285;
 AC AAR72285;
 DT 25-MAR-2003 (revised)
 DT 13-NOV-1995 (first entry)
 XX
 DE Glutamic acid decarboxylase (GAD65) fragment.

XX Glutamic acid decarboxylase; GAD65; autoimmune disorders;
 KM Insulin-dependant diabetes mellitus; stiff man disease.

XX Homo sapiens.

XX WO9507992-A2.

XX 23-MAR-1995.

XX 24-AUG-1994; 94WO-US009478.

XX 17-SEP-1993; 93US-00123859.

XX (REGC) UNIV CALIFORNIA.

XX Tobin AJ, Erlander MG, Kaufman DL, Claessalzler MJ;

XX WPI; 1995-131360/17.

XX New polypeptide fragments of glutamic acid decarboxylase - for diagnosis
 PT and treatment of auto-immune disease, esp. insulin dependant diabetes,
 PT also related nucleic acid, vectors, antibodies, hybridoma(s) etc.

XX Claim 1; Page 76; 100p; English.

XX AAO86481 and AAO86482 encode AAR71733 and AAR79105, rat and human
 CC glutamic acid decarboxylase (GAD65) respectively, from which the GAD65
 CC fragments described in AAR72281-872298 were derived. These fragments can
 CC be used to detect autoantibodies against GAD, e.g. to diagnose and treat
 CC GAD-related autoimmune disorders, such as insulin dependant diabetes
 CC mellitus or stiff man disease. (Updated on 25-MAR-2003 to correct PN
 CC field.) (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 20 AA;

Query Match 1.3%; Score 7; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 227 KWLKSGV 233
 DB 9 KWLKSGV 15

RESULT 52
 AAY59556
 ID AAY59556 standard; peptide; 20 AA.

XX AAY59556;
 AC AAY59556;
 DT 03-APR-2000 (first entry)
 DT
 XX
 DE GAD65 fragment, peptide #25.

XX GAD65; glutamic acid decarboxylase 65; autoimmune disorder; IDDM;
 KM insulin dependant diabetes mellitus; Stiff man disease; diagnosis;
 KM therapy.

XX Homo sapiens.

XX US598366-A.

XX 07-DEC-1999.

XX 09-APR-1997; 97US-00827618.

XX 21-SEP-1990; 90US-00586536.

XX 18-JUN-1991; 91US-00716909.

XX 07-JUN-1995; 95US-00485725.

XX (REGC) UNIV CALIFORNIA.

XX Tobin AJ, Kaufman DL, Erlander MG;

XX WPI; 2000-095930/08.

XX Ameliorating glutamic acid decarboxylase associated autoimmune disorders
 PT such as insulin dependant diabetes mellitus and Stiffman's disease.

XX Claim 1; Col 42; 61p; English.

XX This sequence represents a fragment of the glutamic acid decarboxylase 65
 CC (GAD65) protein. The invention relates to a method of ameliorating GAD
 CC associated autoimmune disorder by administering a GAD65 peptide to the
 CC patient. The method can be used for ameliorating GAD associated
 CC autoimmune disorders such as IDDM (insulin dependant diabetes mellitus)
 CC and Stiff man disease. GAD65 can also be useful for screening drugs that
 CC alter GAD function, for generating monoclonal antibodies and in
 CC immunoassays. GAD65 is an effective diagnostic tool for predicting IDDM
 CC and the diagnosis is quite easy. It is also possible to obtain much
 CC larger quantities of polypeptide via recombinant techniques than are
 CC available from natural sources

XX Sequence 20 AA;

Query Match 1.3%; Score 7; DB 3; Length 20;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 227 KWLKSGV 233
 DB 9 KWLKSGV 15

RESULT 53
 ADC54148
 ID ADC54148 standard; peptide; 26 AA.

XX ADC54148;

XX 18-DEC-2003 (first entry)

XX Peptide linker #3.

XX Peptide linker.

XX Unidentified.

XX JP2003159069-A.

PD 03-JUN-2003.
XX
XX 21-NOV-2001; 2001JP-00356652.
XX
XX 21-NOV-2001; 2001JP-00356652.
XX
XX (KAGA-) KAGAKU GIJYUSU SHINKO JIGYODAN.
PA (KOKU-) KOKURITSU YOSO EISEI KENKYUSHO.
XX
XX WPI; 2003-818676/77.
DR
XX
XX Novel fusion selective marker gene comprising drug-resistance gene
PT coupled to reporter gene, useful for manufacturing recombinant proteins.
XX
XX Example 1; Fig 1; 11pp; Japanese.
PS
XX The present invention relates to a fusion selective marker gene (I)
CC comprising a drug-resistance gene (II) coupled to a reporter gene (III)
CC by a base sequence encoding stuffer amino acid sequence. (II) is a
CC puromycin N-acetyl transferase gene (pac) and (III) is an enhanced green
CC fluorescent protein (EGFP). (I) is useful for manufacturing recombinant
CC protein. (I) is also useful for identifying a desired protein. (I)
CC enables manufacture of recombinant protein, and improved identification
CC of expression of desired gene. The present sequence is a peptide linker
CC which was used to illustrate the invention.
XX
XX Sequence 26 AA;
SQ
Query Match 1.3%; Score 7; DB 7; Length 26;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 337 LEIKLRI 343
DB 4 LEIKLRI 10
RESULT 54
ADM08067
ID ADM08067 standard; peptide; 32 AA.
XX
XX ADM08067;
AC
XX 20-MAY-2004 (first entry)
DT
XX
XX Canine immunoglobulin group 2 lambda VL species framework 3 peptide 33.
DE
XX canine; dog; heavy; immunoglobulin; antibody light chain variable domain;
KW antiallergic; allergy; IGE; gene therapy; group 2 lambda species;
KM VL framework; FR3.
XX
XX Canis familiaris.
OS
XX WO2003060080-A2.
FN
XX 24-JUL-2003.
PD
XX 20-DEC-2002; 2002WO-US041362.
PF
XX 21-DEC-2001; 2001US-0344874P.
PR
XX (IDEX-) IDEXX LAB INC.
PA
XX Krah ER, Guo H, Aiyappa A, Lawton R;
PI
XX WPI; 2003-598521/56.
DR
XX New canine heavy and light chain variable domain polypeptides, useful for
PT treating canine allergy.
PT
XX Claim 34; Page 102; 130pp; English.
PS
XX The invention relates to a novel canine heavy or light chain variable
CC

CC domain polypeptide. The protein of the invention demonstrates
CC antiallergic activity and may be useful for treating canine allergy,
CC possibly via gene therapy. The current sequence is that of a canine
CC immunoglobulin light chain variable domain framework (FR) peptide of the
CC invention.
XX
XX Sequence 32 AA;
SQ
Query Match 1.3%; Score 7; DB 7; Length 32;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 245 GSSATLT 251
DB 12 GSSATLT 18
RESULT 55
ADM08060
ID ADM08060 standard; peptide; 32 AA.
XX
XX ADM08060;
AC
XX 20-MAY-2004 (first entry)
DT
XX
XX Canine immunoglobulin group 2 lambda VL species framework 3 peptide 26.
DE
XX canine; dog; heavy; immunoglobulin; antibody light chain variable domain;
KW antiallergic; allergy; IGE; gene therapy; group 2 lambda species;
KM VL framework; FR3.
XX
XX Canis familiaris.
OS
XX WO2003060080-A2.
PN
XX 24-JUL-2003.
PD
XX 20-DEC-2002; 2002WO-US041362.
PF
XX 21-DEC-2001; 2001US-0344874P.
PR
XX (IDEX-) IDEXX LAB INC.
PA
XX Krah ER, Guo H, Aiyappa A, Lawton R;
PI
XX WPI; 2003-598521/56.
DR
XX New canine heavy and light chain variable domain polypeptides, useful for
PT treating canine allergy.
PT
XX Claim 34; Page 102; 130pp; English.
PS
XX The invention relates to a novel canine heavy or light chain variable
CC domain polypeptide. The protein of the invention demonstrates
CC antiallergic activity and may be useful for treating canine allergy,
CC possibly via gene therapy. The current sequence is that of a canine
CC immunoglobulin light chain variable domain framework (FR) peptide of the
CC invention.
XX
XX Sequence 32 AA;
SQ
Query Match 1.3%; Score 7; DB 7; Length 32;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 245 GSSATLT 251
DB 12 GSSATLT 18
RESULT 56
ADM07905
ID ADM07905 standard; peptide; 32 AA.

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XX ADM07905;
AC (INDEX-) IDEXX LAB INC.
XX PA
XX PI Krah ER, Guo H, Aiyappa A, Lawton R;
XX DR WPI; 2003-598521/56.
XX PT New canine heavy and light chain variable domain polypeptides, useful for
XX PT treating canine allergy.
XX PS Claim 40; Page 107; 130pp; English.
XX CC The invention relates to a novel canine heavy or light chain variable
XX CC domain polypeptide. The protein of the invention demonstrates
XX CC antiallergic activity and may be useful for treating canine allergy,
XX CC possibly via gene therapy. The current sequence is that of a canine
XX CC immunoglobulin light chain variable domain framework (FR) peptide of the
XX CC invention.
XX SQ Sequence 32 AA;
XX
XX Query Match 1.3%; Score 7; DB 7; Length 32;
XX Best Local Similarity 100.0%; Pred. No. 99;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 245 GSSATLT 251
Db 12 GSSATLT 18

RESULT 57
ADM08430
ID ADM08430 standard; peptide; 32 AA.
XX ADM08430;
XX
XX 20-MAY-2004 (first entry)
XX
XX Canine immunoglobulin group 3 VL species framework 3 peptide 15.
XX
XX canine; dog; heavy; immunoglobulin; antibody light chain variable domain;
XX antiallergic; allergy; IGE; gene therapy; group 3 species; VL framework;
XX FR3.
XX
XX Canis familiaris.
XX OS
XX WO2003060080-A2.
XX
XX 24-JUL-2003.
XX
XX 20-DEC-2002; 2002WO-US041362.
XX
XX 21-DEC-2001; 2001US-0344874P.
XX

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XX (INDEX-) IDEXX LAB INC.
XX PA
XX PI Krah ER, Guo H, Aiyappa A, Lawton R;
XX DR WPI; 2003-598521/56.
XX PT New canine heavy and light chain variable domain polypeptides, useful for
XX PT treating canine allergy.
XX PS Claim 40; Page 107; 130pp; English.
XX CC The invention relates to a novel canine heavy or light chain variable
XX CC domain polypeptide. The protein of the invention demonstrates
XX CC antiallergic activity and may be useful for treating canine allergy,
XX CC possibly via gene therapy. The current sequence is that of a canine
XX CC immunoglobulin light chain variable domain framework (FR) peptide of the
XX CC invention.
XX SQ Sequence 32 AA;
XX
XX Query Match 1.3%; Score 7; DB 7; Length 32;
XX Best Local Similarity 100.0%; Pred. No. 99;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 245 GSSATLT 251
Db 12 GSSATLT 18

RESULT 58
ADM08148
ID ADM08148 standard; peptide; 32 AA.
XX ADM08148;
XX
XX 20-MAY-2004 (first entry)
XX
XX Canine immunoglobulin group 2 lambda VL species framework 3 peptide 43.
XX
XX canine; dog; heavy; immunoglobulin; antibody light chain variable domain;
XX antiallergic; allergy; IGE; gene therapy; group 2 lambda species;
XX VL framework; FR3.
XX
XX Canis familiaris.
XX OS
XX WO2003060080-A2.
XX
XX 24-JUL-2003.
XX
XX 20-DEC-2002; 2002WO-US041362.
XX
XX 21-DEC-2001; 2001US-0344874P.
XX
XX (INDEX-) IDEXX LAB INC.
XX
XX Krah ER, Guo H, Aiyappa A, Lawton R;
XX
XX WPI; 2003-598521/56.
XX
XX New canine heavy and light chain variable domain polypeptides, useful for
XX PT treating canine allergy.
XX PS Claim 34; Page 103; 130pp; English.
XX CC The invention relates to a novel canine heavy or light chain variable
XX CC domain polypeptide. The protein of the invention demonstrates
XX CC antiallergic activity and may be useful for treating canine allergy,
XX CC possibly via gene therapy. The current sequence is that of a canine
XX CC immunoglobulin light chain variable domain framework (FR) peptide of the
XX CC invention.
XX SQ Sequence 32 AA;
XX

```

Query Match 1.3%; Score 7; DB 7; Length 32;
 Best Local Similarity 100.0%; Pred. No. 99;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 245 GSSATLT 251
 |||||
 DB 12 GSSATLT 18

RESULT 59

ADM07907
 ID ADM07907 standard; peptide; 32 AA.

AC ADM07907;

DT 20-MAY-2004 (first entry)

DE Canine immunoglobulin group 2 lambda VL genus framework 3 peptide 15.

KM canine; dog; heavy; immunoglobulin; antibody light chain variable domain;

KM antiallergic; allergy; IGE; gene therapy; group 2 lambda genus;

KM VL framework; FR3.

OS Canis familiaris.

PN WO2003060080-A2.

PD 24-JUL-2003.

PF 20-DEC-2002; 2002WO-US041362.

PR 21-DEC-2001; 2001US-0344874P.

PI (IDEX-) IDEXX LAB INC.

PI Krah ER, Guo H, Aiyappa A, Lawton R;

DR WPI; 2003-598521/56.

PT New canine heavy and light chain variable domain polypeptides, useful for

PS treating canine allergy.

PS Claim 33; Page 101; 130pp; English.

CC The invention relates to a novel canine heavy or light chain variable

CC domain polypeptide. The protein of the invention demonstrates

CC antiallergic activity and may be useful for treating canine allergy,

CC possibly via gene therapy. The current sequence is that of a canine

CC immunoglobulin light chain variable domain framework (FR) peptide of the

SQ Sequence 32 AA;

OY 245 GSSATLT 251
 |||||
 DB 12 GSSATLT 18

RESULT 60

ADM07904
 ID ADM07904 standard; peptide; 32 AA.

AC ADM07904;

DT 20-MAY-2004 (first entry)

DE Canine immunoglobulin group 2 lambda VL genus framework 3 peptide 12.

KM canine; dog; heavy; immunoglobulin; antibody light chain variable domain;
 KM antiallergic; allergy; IGE; gene therapy; group 2 lambda genus;
 KM VL framework; FR3.

OS Canis familiaris.

PN WO2003060080-A2.

PD 24-JUL-2003.

PF 20-DEC-2002; 2002WO-US041362.

PR 21-DEC-2001; 2001US-0344874P.

PI (IDEX-) IDEXX LAB INC.

PI Krah ER, Guo H, Aiyappa A, Lawton R;

DR WPI; 2003-598521/56.

PT New canine heavy and light chain variable domain polypeptides, useful for

PS treating canine allergy.

PS Claim 33; Page 101; 130pp; English.

CC The invention relates to a novel canine heavy or light chain variable

CC domain polypeptide. The protein of the invention demonstrates

CC antiallergic activity and may be useful for treating canine allergy,

CC possibly via gene therapy. The current sequence is that of a canine

CC immunoglobulin light chain variable domain framework (FR) peptide of the

SQ Sequence 32 AA;

Query Match 1.3%; Score 7; DB 7; Length 32;
 Best Local Similarity 100.0%; Pred. No. 99;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 245 GSSATLT 251
 |||||
 DB 12 GSSATLT 18

RESULT 61

ADM08347
 ID ADM08347 standard; peptide; 32 AA.

AC ADM08347;

DT 20-MAY-2004 (first entry)

DE Canine immunoglobulin group 3 VL subgenus framework 3 peptide 17.

KM canine; dog; heavy; immunoglobulin; antibody light chain variable domain;

KM antiallergic; allergy; IGE; gene therapy; group 3 subgenus; VL framework;

KM FR3.

OS Canis familiaris.

PN WO2003060080-A2.

PD 24-JUL-2003.

PF 20-DEC-2002; 2002WO-US041362.

PR 21-DEC-2001; 2001US-0344874P.

PI (IDEX-) IDEXX LAB INC.

PI Krah ER, Guo H, Aiyappa A, Lawton R;

DR WPI; 2003-598521/56.

```
PT New canine heavy and light chain variable domain polypeptides, useful for
PT treating canine allergy.
XX
XX Claim 39; Page 106; 130pp; English.
XX
CC The invention relates to a novel canine heavy or light chain variable
CC domain polypeptide. The protein of the invention demonstrates
CC antiallergic activity and may be useful for treating canine allergy,
CC possibly via gene therapy. The current sequence is that of a canine
CC immunoglobulin light chain variable domain framework (FR) peptide of the
CC invention.
XX
SQ Sequence 32 AA;

Query Match 1.3%; Score 7; DB 7; Length 32;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 245 GSSATLT 251
Db 12 GSSATLT 18

RESULT 62
ADM08348
ID ADM08348 standard; peptide; 32 AA.
XX
XX ADM08348;
XX
XX 20-MAY-2004 (first entry)
XX
DE Canine immunoglobulin group 3 VL subgenus framework 3 peptide 18.
XX
XX canine; dog; heavy; immunoglobulin; antibody light chain variable domain;
XX antiallergic; allergy; IGE; gene therapy; group 3 subgenus; VL framework;
XX FR3.
XX
XX Canis familiaris.
XX
XX WO2003060080-A2.
XX
XX 24-JUL-2003.
XX
XX 20-DEC-2002; 2002WO-US041362.
XX
XX 21-DEC-2001; 2001US-0344874P.
XX
XX (IDEX-) IDEXX LAB INC.
XX
XX Krah ER, Guo H, Aiyappa A, Lawton R;
XX
XX WPI; 2003-598521/56.
XX
XX New canine heavy and light chain variable domain polypeptides, useful for
XX treating canine allergy.
XX
XX Claim 39; Page 106; 130pp; English.
XX
XX The invention relates to a novel canine heavy or light chain variable
XX domain polypeptide. The protein of the invention demonstrates
XX antiallergic activity and may be useful for treating canine allergy,
XX possibly via gene therapy. The current sequence is that of a canine
XX immunoglobulin light chain variable domain framework (FR) peptide of the
XX invention.
XX
SQ Sequence 32 AA;

Query Match 1.3%; Score 7; DB 7; Length 32;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 245 GSSATLT 251
Db 12 GSSATLT 18

RESULT 63
ADM08442
ID ADM08442 standard; peptide; 32 AA.
XX
XX ADM08442;
XX
XX 20-MAY-2004 (first entry)
XX
DE Canine immunoglobulin group 3 VL species framework 3 peptide 27.
XX
XX canine; dog; heavy; immunoglobulin; antibody light chain variable domain;
XX antiallergic; allergy; IGE; gene therapy; group 3 species; VL framework;
XX FR3.
XX
XX Canis familiaris.
XX
XX WO2003060080-A2.
XX
XX 24-JUL-2003.
XX
XX 20-DEC-2002; 2002WO-US041362.
XX
XX 21-DEC-2001; 2001US-0344874P.
XX
XX (IDEX-) IDEXX LAB INC.
XX
XX Krah ER, Guo H, Aiyappa A, Lawton R;
XX
XX WPI; 2003-598521/56.
XX
XX New canine heavy and light chain variable domain polypeptides, useful for
XX treating canine allergy.
XX
XX Claim 40; Page 107; 130pp; English.
XX
XX The invention relates to a novel canine heavy or light chain variable
XX domain polypeptide. The protein of the invention demonstrates
XX antiallergic activity and may be useful for treating canine allergy,
XX possibly via gene therapy. The current sequence is that of a canine
XX immunoglobulin light chain variable domain framework (FR) peptide of the
XX invention.
XX
SQ Sequence 32 AA;

Query Match 1.3%; Score 7; DB 7; Length 32;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 245 GSSATLT 251
Db 12 GSSATLT 18

RESULT 64
ADM07910
ID ADM07910 standard; peptide; 32 AA.
XX
XX ADM07910;
XX
XX 20-MAY-2004 (first entry)
XX
DE Canine immunoglobulin group 2 lambda VL genus framework 3 peptide 18.
XX
XX canine; dog; heavy; immunoglobulin; antibody light chain variable domain;
XX antiallergic; allergy; IGE; gene therapy; group 2 lambda genus;
XX VL framework; FR3.
XX
XX Canis familiaris.
XX
XX WO2003060080-A2.
XX
XX
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XX 24-JUL-2003.
PD 20-DEC-2002; 2002WO-US041362.
XX 21-DEC-2001; 2001US-0344874P.
XX (IDEX-) IDEXX LAB INC.
XX Krah ER, Guo H, Aiyappa A, Lawton R;
XX WPI; 2003-598521/56.
DR New canine heavy and light chain variable domain polypeptides, useful for
XX treating canine allergy.
PT Claim 33; Page 101; 130pp; English.
XX The invention relates to a novel canine heavy or light chain variable
XX domain polypeptide. The protein of the invention demonstrates
XX antiallergic activity and may be useful for treating canine allergy,
XX possibly via gene therapy. The current sequence is that of a canine
XX immunoglobulin light chain variable domain framework (FR) peptide of the
XX invention.
SQ Sequence 32 AA;
Query Match 1.3%; Score 7; DB 7; Length 32;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 245 GSSATLT 251
DB 12 GSSATLT 18
RESULT 65
ADM08438
ID ADM08438 standard; peptide; 32 AA.
XX ADM08438;
AC ADM08438;
XX 20-MAY-2004 (first entry)
DT Canine immunoglobulin group 3 VL species framework 3 peptide 23.
XX Canine; dog; heavy; immunoglobulin; antibody light chain variable domain;
XX antiallergic; allergy; IGE; gene therapy; group 3 species; VL framework;
XX FR3.
XX Canis familiaris.
OS WO2003060080-A2.
XX 24-JUL-2003.
PD 20-DEC-2002; 2002WO-US041362.
XX 21-DEC-2001; 2001US-0344874P.
XX (IDEX-) IDEXX LAB INC.
XX Krah ER, Guo H, Aiyappa A, Lawton R;
XX WPI; 2003-598521/56.
DR New canine heavy and light chain variable domain polypeptides, useful for
XX treating canine allergy.
PT Claim 40; Page 107; 130pp; English.
XX The invention relates to a novel canine heavy or light chain variable
XX domain polypeptide. The protein of the invention demonstrates

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```

CC antiallergic activity and may be useful for treating canine allergy,
CC possibly via gene therapy. The current sequence is that of a canine
CC immunoglobulin light chain variable domain framework (FR) peptide of the
CC invention.
XX SQ Sequence 32 AA;
Query Match 1.3%; Score 7; DB 7; Length 32;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 245 GSSATLT 251
DB 12 GSSATLT 18
RESULT 66
ADM08062
ID ADM08062 standard; peptide; 32 AA.
XX ADM08062;
AC ADM08062;
XX 20-MAY-2004 (first entry)
DT Canine immunoglobulin group 2 lambda VL species framework 3 peptide 28.
XX Canine; dog; heavy; immunoglobulin; antibody light chain variable domain;
XX antiallergic; allergy; IGE; gene therapy; group 2 lambda species;
XX VL framework; FR3.
XX Canis familiaris.
OS WO2003060080-A2.
XX 24-JUL-2003.
PD 20-DEC-2002; 2002WO-US041362.
XX 21-DEC-2001; 2001US-0344874P.
XX (IDEX-) IDEXX LAB INC.
XX Krah ER, Guo H, Aiyappa A, Lawton R;
XX WPI; 2003-598521/56.
DR New canine heavy and light chain variable domain polypeptides, useful for
XX treating canine allergy.
XX Claim 34; Page 102; 130pp; English.
XX The invention relates to a novel canine heavy or light chain variable
XX domain polypeptide. The protein of the invention demonstrates
XX antiallergic activity and may be useful for treating canine allergy,
XX possibly via gene therapy. The current sequence is that of a canine
XX immunoglobulin light chain variable domain framework (FR) peptide of the
XX invention.
XX SQ Sequence 32 AA;
Query Match 1.3%; Score 7; DB 7; Length 32;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 245 GSSATLT 251
DB 12 GSSATLT 18
RESULT 67
ADM08336
ID ADM08336 standard; peptide; 32 AA.
XX

```



```

AC ADM08336;
XX
XX 20-MAY-2004 (first entry)
DE Canine immunoglobulin group 3 VL subgenus framework 3 peptide 6.
XX
XX canine; dog; heavy; immunoglobulin; antibody light chain variable domain;
XX antiallergic; allergy; IgE; gene therapy; group 3 subgenus; VL framework;
XX FR3.
XX
XX Canis familiaris.
XX
XX WO2003060080-A2.
XX
XX 24-JUL-2003.
XX
XX 20-DEC-2002; 2002MO-US041362.
XX
XX 21-DEC-2001; 2001US-0344874P.
XX
XX (IDEX-) IDEXX LAB INC.
XX
XX Krah ER, Guo H, Aiyappa A, Lawton R;
XX
XX WPI; 2003-598521/56.
XX
XX PT New canine heavy and light chain variable domain polypeptides, useful for
XX treating canine allergy.
XX
XX PS Claim 39; Page 106; 130pp; English.
XX
XX CC The invention relates to a novel canine heavy or light chain variable
XX domain polypeptide. The protein of the invention demonstrates
XX CC antiallergic activity and may be useful for treating canine allergy,
XX possibly via gene therapy. The current sequence is that of a canine
XX immunoglobulin light chain variable domain framework (FR) peptide of the
XX invention.
XX
XX SQ Sequence 32 AA;
XX
XX Query Match 1.3%; Score 7; DB 7; Length 32;
XX Best Local Similarity 100.0%; Pred. No. 99;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 245 GSSATLT 251
XX |||||
XX 12 GSSATLT 18
XX
XX RESULT 68
XX ADA57203
XX ID ADA57203 standard; protein; 58 AA.
XX
XX AC ADA57203;
XX
XX 20-NOV-2003 (first entry)
XX
XX DE Human secreted protein #486.
XX
XX XX immunosuppressive; antiinflammatory; antiaesthetic; antiallergic;
XX cytoskeletal; cerebroprotective; neuroprotective; nootropic;
XX cardiovascular; antiarteriosclerotic; gene therapy;
XX human secreted protein; immune disorder; inflammation;
XX respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;
XX inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;
XX multiple sclerosis; ischemic brain injury; Parkinson's disease;
XX Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;
XX triple helix formation; antisense gene therapy; forensic biology.
XX
XX OS Homo sapiens.
XX
XX XX WO2002102994-A2.
XX

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PD 27-DEC-2002.
XX
XX 19-MAR-2002; 2002MO-US008278.
XX
XX 21-MAR-2001; 2001US-0277340P.
XX
XX 19-JUL-2001; 2001US-0306171P.
XX
XX 13-NOV-2001; 2001US-0331287P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX PI Rosen CA, Ruben SM;
XX
XX WPI; 2003-167512/16.
XX
XX DR N-PSDB; ADA56307.
XX
XX PT New human secreted polypeptides and polynucleotides, useful for
XX diagnosing, treating or preventing e.g. immune disorders, inflammatory
XX PT conditions, respiratory disorders, cancers, CNS disorders, or
XX neurodegenerative disorders.
XX
XX PS Claim 13; SEQ ID NO 1393; 1754pp; English.
XX
XX CC The invention relates to 592 new human secreted polypeptides useful for
XX diagnosing, treating or preventing e.g. immune disorders, inflammatory
XX CC conditions, respiratory disorders, cancers, CNS disorders, or
XX neurodegenerative disorders, or polypeptides comprising an amino acid
XX sequence at least 95% identical to the new sequences. The polypeptides,
XX antibodies or antibody fragments that bind to the polypeptides, nucleic
XX acids encoding the polypeptides, agonists or antagonists that binds to
XX the polypeptides, are useful in preparing diagnostic or pharmaceutical
XX compositions for diagnosing, treating or preventing an e.g. immune
XX disorder, inflammatory conditions (e.g. inflammatory bowel disease,
XX nephritis or Crohn's disease), respiratory disorders (e.g. asthma and
XX allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
XX (e.g. multiple sclerosis or ischemic brain injury), neurodegenerative
XX disorders (e.g. Parkinson's disease or Alzheimer's disease), and
XX cardiovascular disorders (e.g. atherosclerosis or myocarditis). The
XX polynucleotides are useful for chromosome identification, chromosome
XX mapping, for controlling gene expression through triple helix formation
XX CC or antisense DNA or RNA, in gene therapy, for identifying individuals
XX from minute biological samples, in forensic biology, and as hybridization
XX probes. The polypeptides are useful for as molecular weight markers on
XX sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
XX CC gels, to raise antibodies, for testing biological activities, and for
XX treating or preventing neural disorders, immune system disorders,
XX muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
XX renal, proliferative and/or cancerous diseases. This sequence corresponds
XX CC to one of the polypeptide of the invention. Note: The sequence data for
XX this patent did form part of the printed specification, but was obtained
XX CC in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
XX SQ Sequence 58 AA;
XX
XX Query Match 1.3%; Score 7; DB 6; Length 58;
XX Best Local Similarity 100.0%; Pred. No. 1.7e+02;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 323 AATLPDV 329
XX |||||
XX 43 AATLPDV 49
XX
XX RESULT 69
XX ADA41080
XX ID ADA41080 standard; protein; 58 AA.
XX
XX AC ADA41080;
XX
XX 20-NOV-2003 (first entry)
XX
XX DE Human secreted protein.
XX

```

KW Human; secreted protein; cancer; hyperproliferative disorder;
 KW rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;
 KW anaemia; allergic reaction; asthma; cardiovascular disorder;
 KW wound healing; cytostatic; immunosuppressive; neuroprotective;
 KW antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory;
 KW vulnery; cardiant; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO2002102993-A2.
 XX
 PD 27-DEC-2002.
 XX
 PF 19-MAR-2002; 2002MO-US008123.
 XX
 PR 21-MAR-2001; 2001US-0277340P.
 XX
 PR 19-JUL-2001; 2001US-0306171P.
 XX
 PR 13-NOV-2001; 2001US-0331287P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM;
 XX
 DR WPI; 2003-175238/17.
 XX
 PT New human secreted proteins and nucleic acid molecules, useful for
 XX preparing a diagnostic or pharmaceutical composition for diagnosing,
 PT preventing or treating cancer or other hyperproliferative disorder,
 PT asthma, allergies or AIDS.
 XX
 PS Claim 1; SEQ ID NO 1462; 3205pp; English.
 XX
 CC The invention relates to novel genes ADA39629-ADA4055 and proteins
 CC ADA4056-ADA41501 for human secreted proteins, useful for preventing,
 CC treating or ameliorating medical conditions e.g. by protein or gene
 CC therapy. The polypeptides, nucleic acid molecules, antibodies or their
 CC fragments, and agonists or antagonists that bind to the polypeptide are
 CC useful for preparing a diagnostic or pharmaceutical composition for
 CC diagnosing or treating cancer or other hyperproliferative disorder. The
 CC polypeptides and nucleic acid molecules are also useful for detecting,
 CC preventing, diagnosing, prognosticating, treating or ameliorating cancer
 CC or other hyperproliferative disorders including neoplasms, autoimmune
 CC disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus
 CC erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic
 CC anaemia), haematopoietic or haematological disorders (e.g. anaemia,
 CC thrombocytopenia), allergic reactions including asthma or eczema,
 CC inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory
 CC bowel disease or Crohn's disease), neurodegenerative disorders (e.g.
 CC Alzheimer's disease or Parkinson's disease), cardiovascular disorders
 CC (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,
 CC fungal or viral infections including HIV/AIDS), or wound healing and
 CC disorders of epithelial cell proliferation. The nucleic acids are also
 CC useful for chromosome identification, radiation hybrid mapping or long-
 CC range restriction mapping, as molecular weight markers, or as
 CC hybridization or diagnostic probes. The polypeptides and antibodies are
 CC useful for providing immunological probes for differential identification
 CC of the tissues immunohistochemistry assays. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pcc_sequences.
 CC
 SQ Sequence 58 AA;
 XX

Query Match 1.3%; Score 7; DB 6; Length 58;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 323 ALNLPDV 329
 DB 43 ALNLPDV 49

RESULT 70

ABR47918
 ID ABR47918 standard; protein; 58 AA.
 XX
 AC ABR47918;
 XX
 DT 12-JUN-2003 (first entry)
 XX
 DE Human secreted protein, SEQ ID 809.
 XX
 KW Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic;
 KW vulnery; antiinflammatory; neurotropic; neuroprotective;
 KW antiparkinsonian; gene therapy; human; cardiovascular disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200295010-A2.
 XX
 PD 28-NOV-2002.
 XX
 PF 19-MAR-2002; 2002MO-US009785.
 XX
 PR 21-MAR-2001; 2001US-0277340P.
 XX
 PR 19-JUL-2001; 2001US-0306171P.
 XX
 PR 13-NOV-2001; 2001US-0331287P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM;
 XX
 DR WPI; 2003-129429/12.
 XX
 PT Novel human secreted proteins, useful for detecting, preventing,
 PT diagnosing, prognosticating, treating and/or ameliorating cardiovascular
 PT disorders such as arrhythmia.
 XX
 PS Claim 13; SEQ ID NO 809; 1881pp; English.
 XX
 CC The present invention relates to novel human secreted proteins (ABR47633-
 CC ABR48145) and their coding sequences (ACC50144-ACC50856). The proteins
 CC or their coding sequences are useful for the preparation of a diagnostic
 CC or pharmaceutical composition for diagnosing or treating a cardiovascular
 CC disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary
 CC arteriosclerosis and myocardial ischaemia), neural disorders, immune
 CC system disorders, muscular disorders, reproductive disorders,
 CC gastrointestinal disorders, pulmonary disorders, renal disorders,
 CC proliferative disorders and/or cancerous diseases and conditions, for
 CC wound healing and epithelial cell proliferation, to treat inflammation or
 CC infection, for treating thrombosis and arteriosclerosis, for treating or
 CC preventing neural damage which occurs in neuronal disorders or
 CC neurodegenerative conditions such as Alzheimer's disease and Parkinson's
 CC disease, to enhance bone and periodontal regeneration and aid in tissue
 CC transplants or bone grafts, to prevent skin aging or hair loss, to
 CC stimulate growth and differentiation of haematopoietic cells and bone
 CC marrow cells when used in combination with other cytokines, to maintain
 CC organs before transplantation or for supporting cell culture of primary
 CC tissues, to increase or decrease differentiation or proliferation of
 CC embryonic stem cells, or to modulate mammalian characteristics or
 CC metabolism. Note: The sequence data for this patent was published in
 CC electronic format and is available from WIPO at
 CC ftp.wipo.int/pub/published_pcc_sequences
 CC
 SQ Sequence 58 AA;
 XX

Query Match 1.3%; Score 7; DB 6; Length 58;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 323 ALNLPDV 329
 DB 43 ALNLPDV 49

RESULT 71

AA	AY36325	
ID	AA36325 standard; protein; 59 AA.	
XX		
XX	AA36325;	
XX		
DT	17-SEP-1999 (first entry)	
DE		
XX	Human secreted protein encoded by gene 102.	
KM	Human; secreted protein; cancer; tumour; developmental abnormality;	
KM	fetal deficiency; blood disorder; immune system disorder; inflammation;	
KM	autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;	
KM	schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;	
KM	atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;	
KM	digestive disorder; endocrine disorder; infection; AIDS.	
XX		
OS	Homo sapiens.	
PN		
XX	MO9931117-A1.	
PD		
XX	24-JUN-1999.	
PF		
XX	17-DEC-1998; 98MO-U5027059.	
PR		
XX	18-DEC-1997; 97US-0068006P.	
PR	18-DEC-1997; 97US-0068007P.	
PR	18-DEC-1997; 97US-0068008P.	
PR	18-DEC-1997; 97US-0068003P.	
PR	18-DEC-1997; 97US-00680054P.	
PR	18-DEC-1997; 97US-00680057P.	
PR	18-DEC-1997; 97US-0068064P.	
PR	18-DEC-1997; 97US-0070923P.	
PR	19-DEC-1997; 97US-0068169P.	
PR	19-DEC-1997; 97US-0068365P.	
PR	19-DEC-1997; 97US-0068367P.	
PR	19-DEC-1997; 97US-0068368P.	
PR	19-DEC-1997; 97US-0068369P.	
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
PI		
PI	Moore PA, Ruben SM, Carter KC, Shi Y, Rosen CA, Soppet DR;	
PI	Kyaw H, Wei Y, Florence K, Duan RD, Florence C, Greene JM, Feng P;	
PI	Ferrie AM, Yu G, Janat P, Ni J;	
XX		
DR	WPI; 1999-418745/35.	
XX		
DR	N-PSDB; AAX98017.	
XX		
XX		
PS		
XX	Claim 11; Page 404; 537pp; English.	
CC		
CC	AAX97916 to AAX98029 represent 110 isolated human secreted protein genes	
CC	AAX16224 to AAX16727 represent the secreted proteins encoded by the 110	
CC	human genes. The genes and their corresponding secreted polypeptides are	
CC	useful for preventing, treating or ameliorating medical conditions, e.g.	
CC	by protein or gene therapy. Also pathological conditions can be diagnosed	
CC	by determining the amount of the new polypeptides in a sample or by	
CC	determining the presence of mutations in the new genes. Specific uses are	
CC	described for each of the 110 genes, based on which tissues they are most	
CC	highly expressed in, and include developing products for the diagnosis or	
CC	treatment of cancer, tumours, developmental abnormalities and foetal	
CC	deficiencies, blood disorder, diseases of the immune system, autoimmune	
CC	diseases, inflammation, allergies, Alzheimer's and cognitive disorders,	
CC	schizophrenia, arthritis, asthma, psoriasis, sepsis, skin disorders,	
CC	atherosclerosis, diabetes, cardiovascular disorders, kidney disorders,	
CC	digestive/endocrine disorders, infections and AIDS. The polypeptides are	
CC	also useful for identifying their binding partners. The sequences given	
CC	in AAX97907 to AAX97915 and AAX16223 are used in the exemplification of	
CC	the present invention	
XX		
XX		
50	Sequence 59 AA;	

Best local similarity	100.0%	Pred. No. 1,7e+02;		
Matches	7;	Conservative	0;	Mismatches 0; Indels 0; Gaps

QY	323	ALNLPDV 329	
Db	43	ALNLPDV 49	

RESULT 72	
AAV73500	
ID	AAV73500 standard; protein; 59 AA.
AC	AAV73500;
XX	
DT	29-FEB-2000 (first entry)
DE	Human secreted protein clone ydi53_1 2nd protein sequence SEQ ID NO:268
XX	
KW	Human; secreted protein; immunostimulatory; haemostatic; cytokine;
KM	proliferative; differentiative; chemorectic; chemokineic; vaccine;
XX	thrombolytic; antiinflammatory; cytostatic; immunosuppressive;
XX	gene therapy.
OS	Homo sapiens.
XX	
FN	WC9558642-A2.
XX	
PX	18-NOV-1999.
XX	
PF	14-MAY-1999; 99WC-US010843.
XX	
PR	14-MAY-1998; 98US-0085472P.
PR	17-AUG-1998; 98US-0096824P.
PR	11-SEP-1998; 98US-0099843P.
PR	11-SEP-1998; 98US-0099950P.
PR	15-SEP-1998; 98US-0100424P.
PR	29-OCT-1998; 98US-0102329P.
PR	09-OCT-1998; 98US-0103615P.
PR	11-DEC-1998; 98US-0111799P.
PR	14-DEC-1998; 98US-0112159P.
PR	31-DEC-1998; 98US-0114415P.
PR	10-FEB-1999; 98US-0024805P.
PR	06-APR-1999; 98US-00287150.
PR	13-MAY-1999; 99US-00311021.
XX	
PA	(GENMY) GENETICS INST INC.
XX	
PI	Wong GG, Clark HF, Fechtel K, Agostino MJ;
XX	
DR	WPI; 2000-053095/04.
XX	
PT	Novel polynucleotides and proteins having biological activities which
PT	make them suitable for treating, preventing or ameliorating medical
PT	conditions in humans or animals.
XX	
PS	Disclosure; Page 730; 730pp; English.
XX	

The present invention describes human secreted proteins encoded by polynucleotides obtained from adult testes, foetal brain, adult brain, brain (foetal and adult), foetal kidney, adult spleen, and adult thymus cDNA libraries. The polynucleotides and proteins are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, haemopoiesis regulating activity, tissue growth activity, activin/inhibin activity, chemorectic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, and tumour inhibition activity. The polynucleotides are also stated to be useful for gene therapy. Therapeutic compositions are also presently valuable for veterinary applications. AA252475 to AA25281 encode human secreted proteins, and AAV73390 to AAV73500

CC particularly useful for controlling plant fungal disease, and lessening
 CC the need for artificial agricultural chemicals to protect field crops and
 CC increase crop yield. (I) may also be used as a pharmaceutical compounds
 CC for treating fungal pathogens in humans and animals. AB084698 to AB084744
 CC and ABP55913 to ABP55992 represent sequence used in the exemplification
 CC of the present invention
 XX
 SQ Sequence 63 AA;

Query Match 1.3%; Score 7; DB 6; Length 63;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 352 VLSTSAV 358
 |||||
 Db 14 VLSTSAV 20

RESULT 75

ABP55961
 ID ABP55961 standard; protein; 63 AA.

AC ABP55961;

DT 25-FEB-2003 (first entry)

DE Manduca sexta Fus4 homologue protein SEQ ID NO:76.

XX Antigenic protein; antifungal; haemolymph; fat body; insect larvae;
 KM plant; plant pathogenic fungi; fungicide; gene therapy; fungal pathogen;
 KM plant disease resistance; plant fungal disease.

OS Manduca sexta.

PN WO200286072-A2.

PD 31-OCT-2002.

PF 19-APR-2002; 2002MO-US012511.

PR 20-APR-2001; 2001US-0285355P.

PR 18-APR-2002; 2002US-00125258.

XX
 PA (PION-) PIONEER HI-BRED INT INC.
 (DUPO) DU PONT DE NEMOURS & CO E I.

XX
 PI Altier DJ, Herrmann R, Lu AL, McCutchen BF, Presnail JK;
 PI Weaver JL, Wong JFH;

XX
 DR WPI; 2003-075625/07.
 DR N-PSDB; ABQ84724.

PT New antifungal polypeptides and nucleic acids, useful for enhancing plant
 PT disease resistance to pathogens, particularly resistance of rice, corn or
 PT sunflower, to Magnaportha grisea, Rhizoctonia solani or Fusarium
 PT verticillioides.

PS Claim 9; Page 122; 142pp; English.

XX
 CC The present invention describes antifungal polypeptides (I) isolated from
 CC the haemolymph and fat bodies of insect larvae induced by injection of
 CC plant pathogenic fungi. (I) have plant antifungal and fungicide
 CC activities, and can be used in gene therapy. (II) can be used for
 CC enhancing plant disease resistance to fungal pathogens, particularly
 CC resistance of rice, corn, alfalfa, sunflower, Brassica, soybean, cotton,
 CC safflower, peanut, sorghum, wheat, millet or tobacco to Magnaportha
 CC grisea, Rhizoctonia solani or Fusarium verticillioides. This is
 CC particularly useful for controlling plant fungal disease, and lessening
 CC the need for artificial agricultural chemicals to protect field crops and
 CC increase crop yield. (I) may also be used as a pharmaceutical compounds
 CC for treating fungal pathogens in humans and animals. AB084698 to AB084744
 CC and ABP55913 to ABP55992 represent sequence used in the exemplification
 CC of the present invention

XX
 SQ Sequence 63 AA;

Query Match 1.3%; Score 7; DB 6; Length 63;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 352 VLSTSAV 358
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 Db 14 VLSTSAV 20

Search completed: November 16, 2004, 07:27:34
 Job time : 161 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2004, 07:24:51 ; Search time 142 Seconds

(without alignments)
1300.659 Million cell updates/sec

Title: US-09-927-458-2

Perfect score: 522

Sequence: 1 MRRAVLLKRTWPLEVETE.....DRPPRPGRPRDGLSLM 522

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1568699 seqs, 353819137 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1568699

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

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16: /cgn2_6/ptodata/1/pubppa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep.*
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19: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	522	100.0	522	14	US-10-245-593-2
3	389	74.5	522	16	US-10-679-246-10
4	330	63.2	443	16	US-10-679-246-8
5	271	51.9	317	15	US-10-264-237-2484
6	231	44.3	231	16	US-10-408-765A-752
7	200	38.3	221	14	US-10-094-749-1723
8	200	38.3	462	10	US-09-397-945-200
9	200	38.3	462	15	US-10-264-237-2485
10	200	38.3	462	15	US-10-653-595-200
11	200	38.3	497	10	US-09-397-945-435
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13	128	24.5	174	10	US-09-397-945-434

14	128	24.5	174	15	US-10-653-595-209	Sequence 209, App
15	128	24.5	174	15	US-10-653-595-434	Sequence 434, App
16	128	24.5	175	10	US-09-397-945-209	Sequence 209, App
17	86	16.5	482	13	US-10-042-417-14	Sequence 14, Appl
18	76	14.6	76	14	US-10-029-386-27908	Sequence 27908, A
19	47	9.0	47	14	US-10-029-386-33496	Sequence 33496, A
20	39	7.5	39	13	US-10-042-348-47	Sequence 21, Appl
21	38	7.3	38	11	US-09-801-348-49	Sequence 47, Appl
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23	13	2.5	13	10	US-09-397-945-432	Sequence 432, App
24	13	2.5	13	10	US-09-397-945-433	Sequence 433, App
25	13	2.5	13	15	US-10-653-595-432	Sequence 432, App
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51	7	1.3	63	14	US-10-125-258-76	Sequence 76, Appl
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74	7	1.3	93	9	US-09-764-860-518	Sequence 518, App
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87 7 1.3 109 16 US-10-437-963-126759 Sequence 126759,
 88 7 1.3 113 16 US-10-767-701-50537 Sequence 50537, A
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 90 7 1.3 116 17 US-10-425-115-359734 Sequence 359734,
 91 7 1.3 121 17 US-10-425-115-215265 Sequence 215265,
 92 7 1.3 144 16 US-10-437-963-113263 Sequence 113263,
 93 7 1.3 147 15 US-10-282-1224-72905 Sequence 72905, A
 94 7 1.3 149 17 US-10-425-115-185527 Sequence 185527,
 95 7 1.3 149 16 US-10-437-963-198612 Sequence 198612,
 96 7 1.3 149 16 US-10-767-701-61039 Sequence 61039, A
 97 7 1.3 150 15 US-10-424-599-225222 Sequence 225222,
 98 7 1.3 151 16 US-10-437-963-121948 Sequence 121948,
 99 7 1.3 151 16 US-10-425-115-278362 Sequence 278362,
 100 7 1.3 159 16 US-10-437-963-193530 Sequence 193530,

ALIGNMENTS

RESULT 1
 US-09-927-458-2
 ; Sequence 2, Application US/09927458
 ; Patent No. US20020058024A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WALLACH, David
 ; APPLICANT: KOVALENKO, Andrei
 ; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF RECEPTORS OF THE TNG/NGF RECEPTOR F
 ; FILE REFERENCE: WALLACH=22A
 ; CURRENT APPLICATION NUMBER: US/09/927,458
 ; CURRENT FILING DATE: 2001-08-13
 ; PRIOR APPLICATION NUMBER: PCT/IL98/00125
 ; PRIOR FILING DATE: 1998-03-19
 ; PRIOR APPLICATION NUMBER: IL 120485
 ; PRIOR FILING DATE: 1997-03-19
 ; PRIOR APPLICATION NUMBER: 09/381,358
 ; PRIOR FILING DATE: 1999-09-20
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 522
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-927-458-2

Query Match 100.0%; Score 522; DB 9; Length 522;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLRVLLKRTWPLEVPEPTEPTLGHLSHRLSLCTWGYSSNTFTITLNYKDPITGDE 60
 DB 1 MRLRVLLKRTWPLEVPEPTEPTLGHLSHRLSLCTWGYSSNTFTITLNYKDPITGDE 60

QY 61 ETLASGYIVSGDLICILQDDIPAPNIPSTDSSEHSLQNNQPSLATSSQTSQMODEP 120
 DB 61 ETLASGYIVSGDLICILQDDIPAPNIPSTDSSEHSLQNNQPSLATSSQTSQMODEP 120

QY 121 SDSFGQAAGSGVWDDSMGLSPQNFPEASTIDNNAHMAEGTGFYSEPMGLCSSEVGGVP 180
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RESULT 2
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 ; Sequence 2, Application US/10245593
 ; Publication No. US20030039646A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WALLACH, David
 ; APPLICANT: KOVALENKO, Andrei
 ; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF RECEPTORS OF THE TNG/NGF RECEPTOR F
 ; FILE REFERENCE: WALLACH=22A
 ; CURRENT APPLICATION NUMBER: US/10/245,593
 ; CURRENT FILING DATE: 2002-09-18
 ; PRIOR APPLICATION NUMBER: US/09/927,458
 ; PRIOR FILING DATE: 2001-08-13
 ; PRIOR APPLICATION NUMBER: PCT/IL98/00125
 ; PRIOR FILING DATE: 1998-03-19
 ; PRIOR APPLICATION NUMBER: IL 120485
 ; PRIOR FILING DATE: 1997-03-19
 ; PRIOR APPLICATION NUMBER: 09/381,358
 ; PRIOR FILING DATE: 1999-09-20
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 522
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-245-593-2

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 DB 241 PFCGSSATLTCPVPLGNLIVNATLKINNEISVRLQLPSPFCCKELGNNVANYKD 300

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DB 421 TIFPVNPLHPRPPSRRLPGIIGXYDQPTLPYVGDPISSILPGSTPSQFPPLRP 480
QY 481 RFDVGVGLPGNPLIPRGSGPNDPFRPSRGRPTDRLSFM 522
DB 481 RFDVGVGLPGNPLIPRGSGPNDPFRPSRGRPTDRLSFM 522

RESULT 3

US-10-679-246-10
; Sequence 10, Application US/10679246
; Publication No. US20040163138A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Matsuzawa, Shu-ichi
; TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved
; TITLE OF INVENTION: In Protein Degradation, Products and Methods Related Thereto
; FILE REFERENCE: 66821-235
; CURRENT APPLICATION NUMBER: US/10/679,246
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 09/591,694
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 10
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-679-246-10

Query Match 74.5%; Score 389; DB 16; Length 522;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 489; Conservativity 0; Mismatches 1; Indels 0; Gaps 0;

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DB 33 SLCTWGYSSNTRTITLANKDPLTGDEETLASYGIYSGDILICILLODDIPAPNIPSTD 92
QY 93 SEHSIQLNNEQPSLATSSNOTSMODEQPSDFQCGAAGSVMNDMSMLGPSQNEFEASI 152
DB 93 SEHSIQLNNEQPSLATSSNOTSMODEQPSDFQCGAAGSVMNDMSMLGPSQNEFEASI 152
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QY 393 KELYRKRIHQKESPKGRFVWLTPSSTHTTFFYNNPLHPRPSSRLPGIIGGEYQRP 452
DB 393 KELYRKRIHQKESPKGRFVWLTPSSTHTTFFYNNPLHPRPSSRLPGIIGGEYQRP 452
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DB 453 TLPIYVGDPISSILIPGPTPSQFPPLRPDPVGPPLRGPNDPFRPSRGRPTDRLSFM 512
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DB 513 RPTDGRLSFM 522

RESULT 4

US-10-679-246-8
; Sequence 8, Application US/10679246
; Publication No. US20040163138A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Matsuzawa, Shu-ichi
; TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved
; TITLE OF INVENTION: In Protein Degradation, Products and Methods Related Thereto
; FILE REFERENCE: 66821-235
; CURRENT APPLICATION NUMBER: US/10/679,246
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 09/591,694
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 8
; LENGTH: 443
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-679-246-8

Query Match 63.2%; Score 330; DB 16; Length 443;
Best Local Similarity 99.8%; Pred. No. 6,4e-298;
Matches 430; Conservativity 0; Mismatches 1; Indels 0; Gaps 0;

QY 92 DEHSIQLNNEQPSLATSSNOTSMODEQPSDFQCGAAGSVMNDMSMLGPSQNEFEASI 151
DB 13 DEHSIQLNNEQPSLATSSNOTSMODEQPSDFQCGAAGSVMNDMSMLGPSQNEFEASI 72
QY 152 DNAMAAGTGFYPSPEPMICSESVGEQVPHSLETLTQSDACSDANDALIVLHLMESG 211
DB 73 DNAMAAGTGFYPSPEPMICSESVGEQVPHSLETLTQSDACSDANDALIVLHLMESG 132
QY 212 YIPOGTEAKALMPKMKLSGYVKLQYMHPLCESSATLTCVPLGNLIVNATLKINNEIR 271
DB 133 YIPOGTEAKALMPKMKLSGYVKLQYMHPLCESSATLTCVPLGNLIVNATLKINNEIR 192
QY 272 RSVKRLQLPESFICKELKGENVANITYKDLQKLSLFDQVLYPLAFTROALNLPVFG 331
DB 193 RSVKRLQLPESFICKELKGENVANITYKDLQKLSLFDQVLYPLAFTROALNLPVFG 252
QY 332 VVLPLELKLRIFRLLDVRSVLSAVCRDLFTASNDPLMRFLYLRFRONTYRVQDTW 391
DB 253 VVLPLELKLRIFRLLDVRSVLSAVCRDLFTASNDPLMRFLYLRFRONTYRVQDTW 312
QY 392 WKELYRKRIHQKESPKGRFVWLTPSSTHTTFFYNNPLHPRPSSRLPGIIGGEYQRP 451
DB 313 WKELYRKRIHQKESPKGRFVWLTPSSTHTTFFYNNPLHPRPSSRLPGIIGGEYQRP 372
QY 452 TLPIYVGDPISSILIPGPTPSQFPPLRPDPVGPPLRGPNDPFRPSRGRPTDRLSFM 511
DB 373 TLPIYVGDPISSILIPGPTPSQFPPLRPDPVGPPLRGPNDPFRPSRGRPTDRLSFM 432
QY 512 GRPTDGRLSFM 522
DB 433 GRPTDGRLSFM 443

RESULT 5

US-10-264-237-2484
; Sequence 2484, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131PI
; CURRENT APPLICATION NUMBER: US/10/264,237
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-19
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876

SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO: 2484
LENGTH: 317
TYPE: PRT
ORGANISM: Homo sapiens
US-10-264-237-2484

Query Match 51.9%; Score 271; DB 15; Length 317;
Best Local Similarity 100.0%; Pred. No. 3.5e-243;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 140 LGSQNFPAESIQDVAHAAEGTGFPSPMLCSSESQVQVHSHETTYQASDCSDADAL 199
DB 26 LGSQNFPAESIQDVAHAAEGTGFPSPMLCSSESQVQVHSHETTYQASDCSDADAL 85
QY 200 IYLHLMLESYIPQGTAKALSMPEKMKLSGVYKQLQYHAPLCEGSSATLTCPVPLNLI 259
DB 86 IYLHLMLESYIPQGTAKALSMPEKMKLSGVYKQLQYHAPLCEGSSATLTCPVPLNLI 145
QY 260 VVNAATLKINNEIRSVKRIQLPESFICEKLGENVANIKLOKLSRIFKQQLVYPLIAF 319
DB 146 VVNAATLKINNEIRSVKRIQLPESFICEKLGENVANIKLOKLSRIFKQQLVYPLIAF 205
QY 320 TROALNLPDVFGLVYLPLELKIRIFRLDVSVLSAVCRDLFTASNDPLMRFVLYARD 379
DB 206 TROALNLPDVFGLVYLPLELKIRIFRLDVSVLSAVCRDLFTASNDPLMRFVLYARD 265
QY 380 FRDNTVRVODTDWKELYKRRHIORKESPGR 410
DB 266 FRDNTVRVODTDWKELYKRRHIORKESPGR 296

RESULT 6

US-10-408-765A-752
Sequence 752, Application US/10408765A
Publication No. US20040101874A1
GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Fathy, Eoin D.
APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary W.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 752
LENGTH: 231
TYPE: PRT
ORGANISM: Homo sapiens
US-10-408-765A-752

Query Match 44.3%; Score 231; DB 16; Length 231;
Best Local Similarity 100.0%; Pred. No. 4.2e-206;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 232 ENVANITYDLOKLSLRFQOLVYPLATTRQALNLPVFGVYLPLEKIRIFRLDVS 351
DB 1 ENVANITYDLOKLSLRFQOLVYPLATTRQALNLPVFGVYLPLEKIRIFRLDVS 60
QY 352 VLSAVCRDLFTASNDPLMRFVLYLPDVFGLVYLPLEKIRIFRLDVS 411
DB 61 VLSAVCRDLFTASNDPLMRFVLYLPDVFGLVYLPLEKIRIFRLDVS 120
QY 412 VMLPSSHTIIPFYNPLHPRPFGSRPLPGIIGGEYDQRTLPYVGPPISSSLIPGGET 471
DB 121 VMLPSSHTIIPFYNPLHPRPFGSRPLPGIIGGEYDQRTLPYVGPPISSSLIPGGET 180

QY 472 PSQFPELRPRFDPVGPPLPGPNPILPGRGPNDRPFPFRSGRPTDGRLSFM 522
DB 181 PSQFPELRPRFDPVGPPLPGPNPILPGRGPNDRPFPFRSGRPTDGRLSFM 231

RESULT 7

US-10-094-749-1723
Sequence 1723, Application US/10094749
Publication No. US20030219741A1
GENERAL INFORMATION:
APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAYASU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHICO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOMYUKI
APPLICANT: NAGAHARA, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328361
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1723
LENGTH: 221
TYPE: PRT
ORGANISM: Homo sapiens
US-10-094-749-1723

Query Match 38.3%; Score 200; DB 14; Length 221;
Best Local Similarity 100.0%; Pred. No. 2.8e-177;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 323 AMLPVPFGLVYLPLELKIRIFRLDVSVLSAVCRDLFTASNDPLMRFVLYARD 382
DB 22 AMLPVPFGLVYLPLELKIRIFRLDVSVLSAVCRDLFTASNDPLMRFVLYARD 81
QY 383 NTVRVODTDWKELYKRRHIORKESPGRFVMLPSTHTIIPFYNPLHPRPFGSRPLPG 442
DB 82 NTVRVODTDWKELYKRRHIORKESPGRFVMLPSTHTIIPFYNPLHPRPFGSRPLPG 141
QY 443 IIGGEYDQRTLPYVGPPISSSLIPGGETSQFPPLRPFDFVGPLPGPNPILPGRGPN 502
DB 142 IIGGEYDQRTLPYVGPPISSSLIPGGETSQFPPLRPFDFVGPLPGPNPILPGRGPN 201
QY 503 DRPFRPSRGRPTDGRLSFM 522
DB 202 DRPFRPSRGRPTDGRLSFM 221

RESULT 8

US-09-397-945-200
Sequence 200, Application US/09397945
Publication No. US20030065139A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc. et al.
TITLE OF INVENTION: 95 Human secreted proteins
FILE REFERENCE: P2027P1

CURRENT APPLICATION NUMBER: US/09/397,945
CURRENT FILING DATE: 1999-09-17
PRIORITY APPLICATION NUMBER: PCT/US99/05804
PRIORITY FILING DATE: 1999-03-18
PRIORITY APPLICATION NUMBER: 60/078,566
PRIORITY FILING DATE: 1998-03-19
PRIORITY APPLICATION NUMBER: 60/078,576
PRIORITY FILING DATE: 1998-03-19
PRIORITY APPLICATION NUMBER: 60/078,573
PRIORITY FILING DATE: 1998-03-19
PRIORITY APPLICATION NUMBER: 60/078,574
PRIORITY FILING DATE: 1998-03-19
PRIORITY APPLICATION NUMBER: 60/078,579
PRIORITY FILING DATE: 1998-03-19
PRIORITY APPLICATION NUMBER: 60/080,314
PRIORITY FILING DATE: 1998-04-01
PRIORITY APPLICATION NUMBER: 60/080,312
PRIORITY FILING DATE: 1998-04-01
PRIORITY APPLICATION NUMBER: 60/078,578
PRIORITY FILING DATE: 1998-03-19
PRIORITY APPLICATION NUMBER: 60/078,581
PRIORITY FILING DATE: 1998-03-19
PRIORITY APPLICATION NUMBER: 60/078,577
PRIORITY FILING DATE: 1998-03-19
PRIORITY APPLICATION NUMBER: 60/078,563
PRIORITY FILING DATE: 1998-03-19
PRIORITY APPLICATION NUMBER: 60/080,313
PRIORITY FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 470
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 200
LENGTH: 462
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (115)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-397-945-200

Query Match 38.3%; Score 200; DB 10; Length 462;
Best Local Similarity 100.0%; Pred. No. 5.2e-177;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 323 ALNLPDVGVLVLPLELKRIFRLDVRVSLSAVCRDLFTASNDPLMRFLYLRDPRD 382
DB 263 ALNLPDVGVLVLPLELKRIFRLDVRVSLSAVCRDLFTASNDPLMRFLYLRDPRD 322
QY 383 NTVAVQDTWKELYRKRIQRKESPKGRFVWLTPSSHTTTPFYNNPLHPPFPSSRLPPG 442
DB 323 NTVAVQDTWKELYRKRIQRKESPKGRFVWLTPSSHTTTPFYNNPLHPPFPSSRLPPG 382
QY 443 IIGGEYDQRPPLPYVGDPISSLPGGGETPSQFPPLRPDPVGLPGPNILPGRGGPN 502
DB 383 IIGGEYDQRPPLPYVGDPISSLPGGGETPSQFPPLRPDPVGLPGPNILPGRGGPN 442
QY 503 DRPFPRPSRGRPTDGRLSFM 522
DB 443 DRPFPRPSRGRPTDGRLSFM 462

RESULT 9
US-10-264-237-2485
Sequence 2485, Application US/10264237
Publication No. US20040009491A1
GENERAL INFORMATION:
APPLICANT: Bize et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA131P1
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
PRIORITY APPLICATION NUMBER: PCT/US01/16450
PRIORITY FILING DATE: 2001-05-18

PRIORITY APPLICATION NUMBER: US 60/205,515
PRIORITY FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2876
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 2485
LENGTH: 462
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (115)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-237-2485

Query Match 38.3%; Score 200; DB 15; Length 462;
Best Local Similarity 100.0%; Pred. No. 5.2e-177;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 323 ALNLPDVGVLVLPLELKRIFRLDVRVSLSAVCRDLFTASNDPLMRFLYLRDPRD 382
DB 263 ALNLPDVGVLVLPLELKRIFRLDVRVSLSAVCRDLFTASNDPLMRFLYLRDPRD 322
QY 383 NTVAVQDTWKELYRKRIQRKESPKGRFVWLTPSSHTTTPFYNNPLHPPFPSSRLPPG 442
DB 323 NTVAVQDTWKELYRKRIQRKESPKGRFVWLTPSSHTTTPFYNNPLHPPFPSSRLPPG 382
QY 443 IIGGEYDQRPPLPYVGDPISSLPGGGETPSQFPPLRPDPVGLPGPNILPGRGGPN 502
DB 383 IIGGEYDQRPPLPYVGDPISSLPGGGETPSQFPPLRPDPVGLPGPNILPGRGGPN 442
QY 503 DRPFPRPSRGRPTDGRLSFM 522
DB 443 DRPFPRPSRGRPTDGRLSFM 462

RESULT 10
US-10-653-595-200
Sequence 200, Application US/10653595
Publication No. US20040048304A1
GENERAL INFORMATION:
APPLICANT: Ruben et. al.
TITLE OF INVENTION: 95 Human secreted proteins
FILE REFERENCE: P2027P1C1
CURRENT APPLICATION NUMBER: US/10/653,595
CURRENT FILING DATE: 2003-09-03
PRIORITY APPLICATION NUMBER: US 09/397945
PRIORITY FILING DATE: 1999-09-17
PRIORITY APPLICATION NUMBER: PCT/US99/05804
PRIORITY FILING DATE: 1999-03-18
PRIORITY APPLICATION NUMBER: 60/078,566
PRIORITY FILING DATE: 1998-03-19
PRIORITY APPLICATION NUMBER: 60/078,576
PRIORITY FILING DATE: 1998-03-19
PRIORITY APPLICATION NUMBER: 60/078,573
PRIORITY FILING DATE: 1998-03-19
PRIORITY APPLICATION NUMBER: 60/078,574
PRIORITY FILING DATE: 1998-03-19
PRIORITY APPLICATION NUMBER: 60/078,579
PRIORITY FILING DATE: 1998-03-19
PRIORITY APPLICATION NUMBER: 60/080,314
PRIORITY FILING DATE: 1998-04-01
PRIORITY APPLICATION NUMBER: 60/080,312
PRIORITY FILING DATE: 1998-04-01
PRIORITY APPLICATION NUMBER: 60/078,578
PRIORITY FILING DATE: 1998-03-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 470
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 200
LENGTH: 462
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:

QY 383 NTVRVQDTDWKEIYRKXHIQKESPKGRFVMLPSSSTHTIPFYNNPLHPRPSSRLPG 442
DB 358 NTVRVQDTDWKEIYRKXHIQKESPKGRFVMLPSSSTHTIPFYNNPLHPRPSSRLPG 417
QY 443 IIGGEYDQRTPLPYVGPDISLIPGGEPTSPQFPPLRPDPVGPLGPNPILPGRGPN 502
DB 418 IIGGEYDQRTPLPYVGPDISLIPGGEPTSPQFPPLRPDPVGPLGPNPILPGRGPN 477
QY 503 DRPPFRPSRGRPTDGRLSFM 522
DB 478 DRPPFRPSRGRPTDGRLSFM 497

RESULT 13
US-09-397-945-434
Sequence 434, Application US/09397945
Publication No. US20030065139A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc. et al.
TITLE OF INVENTION: 95 Human secreted proteins
FILE REFERENCE: P2027P1
CURRENT APPLICATION NUMBER: US/09/397,945
PRIOR FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: PCT/US99/05804
PRIOR FILING DATE: 1999-03-18
PRIOR APPLICATION NUMBER: 60/078,566
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,576
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,573
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,574
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,579
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/080,314
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080,312
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/078,578
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,581
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,577
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,563
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/080,313
PRIOR FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 470
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 434
LENGTH: 174
TYPE: PRT
ORGANISM: Homo sapiens
US-09-397-945-434

Query Match 24.5%, Score 128, DB 10, Length 174;
Best Local Similarity 100.0%, Pred. No. 2e-110;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 395 LYRKXHIQKESPKGRFVMLPSSSTHTIPFYNNPLHPRPSSRLPGIIGGEYDQRTPL 454
DB 47 LYRKXHIQKESPKGRFVMLPSSSTHTIPFYNNPLHPRPSSRLPGIIGGEYDQRTPL 106
QY 455 PYVGPDISLIPGGEPTSPQFPPLRPDPVGPLGPNPILPGRGPNDRPFRPSRGRP 514
DB 107 PYVGPDISLIPGGEPTSPQFPPLRPDPVGPLGPNPILPGRGPNDRPFRPSRGRP 166
QY 515 TDGRLSFM 522
DB 167 TDGRLSFM 174

RESULT 14
US-10-653-595-209
Sequence 209, Application US/10653595
Publication No. US20040048304A1
GENERAL INFORMATION:
APPLICANT: Ruben et. al.
TITLE OF INVENTION: 95 Human secreted proteins
FILE REFERENCE: P2027P1C1
CURRENT APPLICATION NUMBER: US/10/653,595
CURRENT FILING DATE: 2003-09-03
PRIOR APPLICATION NUMBER: US 09/397945
PRIOR FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: PCT/US99/05804
PRIOR FILING DATE: 1999-03-18
PRIOR APPLICATION NUMBER: 60/078,566
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,576
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,573
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,574
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,579
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/080,314
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080,312
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/078,578
PRIOR FILING DATE: 1998-03-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 470
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 209
LENGTH: 174
TYPE: PRT
ORGANISM: Homo sapiens
US-10-653-595-209

Query Match 24.5%, Score 128, DB 15, Length 174;
Best Local Similarity 100.0%, Pred. No. 2e-110;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 395 LYRKXHIQKESPKGRFVMLPSSSTHTIPFYNNPLHPRPSSRLPGIIGGEYDQRTPL 454
DB 47 LYRKXHIQKESPKGRFVMLPSSSTHTIPFYNNPLHPRPSSRLPGIIGGEYDQRTPL 106
QY 455 PYVGPDISLIPGGEPTSPQFPPLRPDPVGPLGPNPILPGRGPNDRPFRPSRGRP 514
DB 107 PYVGPDISLIPGGEPTSPQFPPLRPDPVGPLGPNPILPGRGPNDRPFRPSRGRP 166
QY 515 TDGRLSFM 522
DB 167 TDGRLSFM 174

RESULT 15
US-10-653-595-434
Sequence 434, Application US/10653595
Publication No. US20040048304A1
GENERAL INFORMATION:
APPLICANT: Ruben et. al.
TITLE OF INVENTION: 95 Human secreted proteins
FILE REFERENCE: P2027P1C1
CURRENT APPLICATION NUMBER: US/10/653,595
CURRENT FILING DATE: 2003-09-03
PRIOR APPLICATION NUMBER: US 09/397945
PRIOR FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: PCT/US99/05804
PRIOR FILING DATE: 1999-03-18
PRIOR APPLICATION NUMBER: 60/078,566
PRIOR FILING DATE: 1998-03-19

PRIOR APPLICATION NUMBER: 60/078,576
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,573
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,574
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,579
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/080,314
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080,312
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/078,578
PRIOR FILING DATE: 1998-03-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 470
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 434
LENGTH: 174
TYPE: PRT
ORGANISM: Homo sapiens
US-10-653-595-434

Query Match 24.5% Score 128; DB 15; Length 174;
Best Local Similarity 100.0%; Pred. No. 2e-110;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 395 LYRKHIQKESPKGRFVWLLPSSSTHTIPFYNNPLHRRPFPSSRLPGIIGEXYDQPTL 454
DB 47 LYRKHIQKESPKGRFVWLLPSSSTHTIPFYNNPLHRRPFPSSRLPGIIGEXYDQPTL 106
QY 455 PYVGPDISLLPGPGETSQFPPLRPDPVGPPLGPNPILPGRGPNDRFPFRSGRP 514
DB 107 PYVGPDISLLPGPGETSQFPPLRPDPVGPPLGPNPILPGRGPNDRFPFRSGRP 166
QY 515 TDGRLSFM 522
DB 167 TDGRLSFM 174

RESULT 16
US-09-397-945-209
Sequence 209, Application US/09397945
Publication No. US20030065139A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc. et al.
TITLE OF INVENTION: 95 Human secreted proteins
FILE REFERENCE: P2027P1
CURRENT FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: US/09/397,945
PRIOR FILING DATE: 1999-03-18
PRIOR APPLICATION NUMBER: 60/078,566
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,576
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,573
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,574
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,579
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/080,314
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080,312
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/078,578
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,581
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,577
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,563

PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/080,313
PRIOR FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 470
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 209
LENGTH: 175
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (175)
OTHER INFORMATION: Xaa equals stop translation
US-09-397-945-209

Query Match 24.5% Score 128; DB 10; Length 175;
Best Local Similarity 100.0%; Pred. No. 2e-110;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 395 LYRKHIQKESPKGRFVWLLPSSSTHTIPFYNNPLHRRPFPSSRLPGIIGEXYDQPTL 454
DB 47 LYRKHIQKESPKGRFVWLLPSSSTHTIPFYNNPLHRRPFPSSRLPGIIGEXYDQPTL 106
QY 455 PYVGPDISLLPGPGETSQFPPLRPDPVGPPLGPNPILPGRGPNDRFPFRSGRP 514
DB 107 PYVGPDISLLPGPGETSQFPPLRPDPVGPPLGPNPILPGRGPNDRFPFRSGRP 166
QY 515 TDGRLSFM 522
DB 167 TDGRLSFM 174

RESULT 17
US-10-042-417-14
Sequence 14, Application US/10042417
Publication No. US20020123082A1
GENERAL INFORMATION:
APPLICANT: Pacano, M.
TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF
PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS
FILE REFERENCE: 5914-090-999
CURRENT APPLICATION NUMBER: US/10/042,417
CURRENT FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: 60/260,179
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 482
TYPE: PRT
ORGANISM: Homo sapiens
US-10-042-417-14

Query Match 16.5% Score 86; DB 13; Length 482;
Best Local Similarity 100.0%; Pred. No. 5.6e-71;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 LCEGSSATLTCTVPLGNLIVNNAATLKINNEISVYRIQLPSPFICKELGENVANIYDYL 301
DB 202 LCEGSSATLTCTVPLGNLIVNNAATLKINNEISVYRIQLPSPFICKELGENVANIYDYL 261
QY 302 QXLSRLPKDQIVYPLAFTROLNLP 327
DB 262 QXLSRLPKDQIVYPLAFTROLNLP 287

RESULT 18
US-10-029-386-27908
Sequence 27908, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 27908
LENGTH: 76
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO CHR22.55.0
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2
OTHER INFORMATION: SWISSPROT HIT: Q9Y311, EVALUE 5.00e-39
US-10-029-386-27908

Query Match 14.6%; Score 76; DB 14; Length 76;
Best Local Similarity 100.0%; Pred. No. 2.3e-62;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 140 LGPSONEFEASIODNMAHAGTGFPSEPMLCSESVCVPSLETLYOSADCSNDAL 199
Db 1 LGPSONEFEASIODNMAHAGTGFPSEPMLCSESVCVPSLETLYOSADCSNDAL 60

Qy 200 IVLIHLMLESGYIPQ 215
Db 61 IVLIHLMLESGYIPQ 76

RESULT 19
US-10-029-386-33496
Sequence 33496, Application US/100293386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 33496
LENGTH: 47
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL035068.3
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7
OTHER INFORMATION: SWISSPROT HIT: Q9Y311, EVALUE 5.00e-22
US-10-029-386-33496

Query Match 9.0%; Score 47; DB 14; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.4e-35;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 216 GTEKALSMPEKMLSGVYKLYQHNPCESSATLTVCPLGNILYVN 262
Db 1 GTEKALSMPEKMLSGVYKLYQHNPCESSATLTVCPLGNILYVN 47

RESULT 20
US-10-042-417-21

Sequence 21, Application US/10042417
Publication No. US20020123082A1
GENERAL INFORMATION:
APPLICANT: Pagano, M.
TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF
FILE REFERENCE: PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS
CURRENT APPLICATION NUMBER: US/10/042,417
CURRENT FILING DATE: 2002-01-07
PRIORITY FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21
LENGTH: 39
TYPE: PRT
ORGANISM: Homo sapiens
US-10-042-417-21

Query Match 7.5%; Score 39; DB 13; Length 39;
Best Local Similarity 100.0%; Pred. No. 3.3e-28;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 335 LPELKLRIIFRLDVRVSLSSAVCRDLFTASNDPLMR 373
Db 1 LPELKLRIIFRLDVRVSLSSAVCRDLFTASNDPLMR 39

RESULT 21
US-09-801-348-47
Sequence 47, Application US/09801348
Publication No. US20040166530A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeffrey W.
APPLICANT: Elledge, Stephen J.
TITLE OF INVENTION: P-BOX PROTEINS AND GENES
FILE REFERENCE: BCM-03510
CURRENT APPLICATION NUMBER: US/09/801,348
CURRENT FILING DATE: 2001-07-31
EARLIER APPLICATION NUMBER: 09/172,841
EARLIER FILING DATE: 1998-10-15
EARLIER APPLICATION NUMBER: 08/951,621
EARLIER FILING DATE: 1997-10-16
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 47
LENGTH: 38
TYPE: PRT
ORGANISM: Homo sapiens
US-09-801-348-47

Query Match 7.3%; Score 38; DB 11; Length 38;
Best Local Similarity 100.0%; Pred. No. 2.7e-27;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 335 LPELKLRIIFRLDVRVSLSSAVCRDLFTASNDPLMR 372
Db 1 LPELKLRIIFRLDVRVSLSSAVCRDLFTASNDPLMR 38

RESULT 22
US-09-801-348-49
Sequence 49, Application US/09801348
Publication No. US20040166530A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeffrey W.
APPLICANT: Elledge, Stephen J.
TITLE OF INVENTION: P-BOX PROTEINS AND GENES
FILE REFERENCE: BCM-03510
CURRENT APPLICATION NUMBER: US/09/801,348
CURRENT FILING DATE: 2001-07-31
EARLIER APPLICATION NUMBER: 09/172,841
EARLIER FILING DATE: 1998-10-15

```
;; EARLIER APPLICATION NUMBER: 08/951,621
;; EARLIER FILING DATE: 1997-10-16
;; NUMBER OF SEQ ID NOS: 60
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO: 49
;; LENGTH: 38
;; TYPE: PRT
;; ORGANISM: Mus musculus
US-09-801-348-49
```

```
Query Match      2.9%; Score 15; DB 11; Length 38;
Best Local Similarity 100.0%; Pred. No. 6.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      335 LPLELKLRIFFRLDLY 349
DB      1 LPLELKLRIFFRLDLY 15
```

```
RESULT 23
US-09-397-945-432
; Sequence 432, Application US/09397945
; Publication No. US20030065139A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: 95 Human secreted proteins
; FILE REFERENCE: P2027P1
; CURRENT FILING DATE: US/09/397,945
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: PCT/US99/05804
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/078,566
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,576
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,573
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,574
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,579
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/080,314
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080,312
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/078,578
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,581
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,577
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,563
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/080,313
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 470
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 432
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-397-945-432
```

```
Query Match      2.5%; Score 13; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      308 FKQDLVYPLAFT 320
DB      1 FKQDLVYPLAFT 13
```

RESULT 24

```
US-09-397-945-433
; Sequence 433, Application US/09397945
; Publication No. US20030065139A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: 95 Human secreted proteins
; FILE REFERENCE: P2027P1
; CURRENT FILING DATE: US/09/397,945
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: PCT/US99/05804
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/078,566
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,576
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,573
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,574
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,579
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/080,314
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080,312
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/078,578
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,581
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,577
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,563
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/080,313
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 470
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 433
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-397-945-433
```

```
Query Match      2.5%; Score 13; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      321 RQALNLPDVFGLV 333
DB      1 RQALNLPDVFGLV 13
```

```
RESULT 25
US-10-653-595-432
; Sequence 432, Application US/10653595
; Publication No. US20040048504A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et. al.
; TITLE OF INVENTION: 95 Human secreted proteins
; FILE REFERENCE: P2027P1
; CURRENT FILING DATE: US/10/653,595
; CURRENT FILING DATE: 2003-09-03
; PRIOR APPLICATION NUMBER: US 09/397945
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: PCT/US99/05804
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/078,566
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,576
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,573
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,574
```


PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,579
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/080,314
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080,312
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/078,578
PRIOR FILING DATE: 1998-03-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 470
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 432
LENGTH: 13
TYPE: PRT
ORGANISM: Homo sapiens
US-10-653-595-432

Query Match 2.5%; Score 13; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 308 FKDQVYPLAFT 320
Db 1 FKDQVYPLAFT 13

RESULT 26
US-10-653-595-433
Sequence 433, Application US/10653595
Publication No. US20040048304A1
GENERAL INFORMATION:
APPLICANT: Ruben et. al.
TITLE OF INVENTION: 95 Human secreted proteins
FILE REFERENCE: P2027P1C1
CURRENT APPLICATION NUMBER: US/10/653,595
CURRENT FILING DATE: 2003-09-03
PRIOR APPLICATION NUMBER: US 09/397945
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: PCT/US99/05804
PRIOR FILING DATE: 1999-03-18
PRIOR APPLICATION NUMBER: 60/078,566
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,576
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,573
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,574
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,579
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/080,314
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080,312
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/078,578
PRIOR FILING DATE: 1998-03-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 470
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 433
LENGTH: 13
TYPE: PRT
ORGANISM: Homo sapiens
US-10-653-595-433

Query Match 2.5%; Score 13; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 321 ROALNLPDVFGLV 333
Db 1 ROALNLPDVFGLV 13

RESULT 27
US-09-764-891-2898
Sequence 2898, Application US/09764891
Publication No. US2003007808A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PCC06
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2898
LENGTH: 57
TYPE: PRT
ORGANISM: Homo sapiens
US-09-764-891-2898

Query Match 1.5%; Score 8; DB 10; Length 57;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 406 SPKGRFVM 413
Db 1 SPKGRFVM 8

RESULT 28
US-10-029-386-29488
Sequence 29488, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Penn, Sharon G.
APPLICANT: Hanel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR CH
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 29488
LENGTH: 63
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO CHRA.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.45
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.4
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.59
OTHER INFORMATION: SWISSPROT HIT: P22599, EVALUATE 1.60e+00
US-10-029-386-29488

Query Match 1.5%; Score 8; DB 14; Length 63;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 350 RSVLSLSA 357
Db 32 RSVLSLSA 39

RESULT 29
US-10-425-115-355684
Sequence 355684, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.

```

; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 355684
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_87549C.1.pep
US-10-425-115-355684

Query Match
Best Local Similarity 1.5%; Score 8; DB 17; Length 72;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 199 LIVLHLL 206
DB 39 LIVLHLL 46

RESULT 30
US-10-424-599-272597
; Sequence 272597, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 272597
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_88177C.1.pep
US-10-424-599-272597

Query Match
Best Local Similarity 1.5%; Score 8; DB 15; Length 81;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 PETEPTLG 24
DB 58 PETEPTLG 65

RESULT 31
US-10-437-963-142276
; Sequence 142276, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
```

```

; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 142276
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_43298C.1.pep
US-10-437-963-142276

Query Match
Best Local Similarity 1.5%; Score 8; DB 16; Length 89;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 494 ILPGRGSP 501
DB 55 ILPGRGSP 62

RESULT 32
US-10-424-599-277325
; Sequence 277325, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 277325
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(102)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_92448C.1.pep
US-10-424-599-277325

Query Match
Best Local Similarity 1.5%; Score 8; DB 15; Length 102;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 380 FRDNTVRV 387
DB 43 FRDNTVRV 50

RESULT 33
US-10-425-115-193389
; Sequence 193389, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 193389
; LENGTH: 102
```

TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MFT4577_107956C.1.pep
US-10-425-115-193389

Query Match
Best Local Similarity 100.0%; Score 8; DB 17; Length 102;
Pred. No. 51;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 341 LRIIRLLD 348
DB 41 LRIIRLLD 48

RESULT 34
US-10-425-115-322444
Sequence 322444, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yinhua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 322444
LENGTH: 117
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MFT4577_57133C.1.pep
US-10-425-115-322444

Query Match
Best Local Similarity 100.0%; Score 8; DB 17; Length 117;
Pred. No. 57;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 349 VRSVLSLS 356
DB 57 VRSVLSLS 64

RESULT 35
US-10-369-493-4506
Sequence 4506, Application US/10369493
Publication No. US2003023675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 4506
LENGTH: 478
TYPE: PRT
ORGANISM: Burkholderia fungorum
US-10-369-493-4506

Query Match
Best Local Similarity 100.0%; Score 8; DB 14; Length 478;
Pred. No. 1.9e+02;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 216 GTEAKALS 223
DB 388 GTEAKALS 395

RESULT 36
US-10-369-493-7264
Sequence 7264, Application US/10369493
Publication No. US2003023675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 7264
LENGTH: 478
TYPE: PRT
ORGANISM: Burkholderia cepacia
US-10-369-493-7264

Query Match
Best Local Similarity 100.0%; Score 8; DB 14; Length 478;
Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 216 GTEAKALS 223
DB 388 GTEAKALS 395

RESULT 37
US-09-795-671-5
Sequence 5, Application US/09795671
Publication No. US20030207347A1
GENERAL INFORMATION:
APPLICANT: Burgess, Robert
APPLICANT: Brunken, William
APPLICANT: Koch, Manuel
APPLICANT: Hunter, Dale
APPLICANT: Olson, Pamela
TITLE OF INVENTION: BETA NETRIN AND USES THEREOF
FILE REFERENCE: 10287-057001
CURRENT APPLICATION NUMBER: US/09/795,671
CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 60/185,811
PRIOR FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: US 60/229,893
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 628
TYPE: PRT
ORGANISM: Mus musculus
US-09-795-671-5

Query Match
Best Local Similarity 100.0%; Score 8; DB 10; Length 628;
Pred. No. 2.4e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LRVRLIKR 10
DB 224 LRVRLIKR 231

RESULT 38
US-10-282-122A-49250
; Sequence 49250, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282.122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/205,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49250
; LENGTH: 789
; TYPE: PRT
; ORGANISM: Burkholderia fungorum
US-10-282-122A-49250

Query Match 1.5%; Score 8; DB 15; Length 789;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 324 INLPDVF 331
DB 727 INLPDVF 734

RESULT 39
US-10-327-598-188
; Sequence 188, Application US/10327598
; Publication No. US20040181039A1
; GENERAL INFORMATION:
; APPLICANT: Krah, Eugene
; APPLICANT: Guo, Honliang
; APPLICANT: Aiyeppa, Ashok
; APPLICANT: Lawton, Robert
; TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and
; TITLE OF INVENTION: for Making and Using Them
; FILE REFERENCE: 01-799-A

; CURRENT APPLICATION NUMBER: US/10/327,598
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/344,874
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 1139
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 188
; LENGTH: 32
; TYPE: PRT
; ORGANISM: canis familiaris;
US-10-327-598-188

Query Match 1.3%; Score 7; DB 16; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 GSSATLT 251
DB 12 GSSATLT 18

RESULT 40
US-10-327-598-190
; Sequence 190, Application US/10327598
; Publication No. US20040181039A1
; GENERAL INFORMATION:
; APPLICANT: Krah, Eugene
; APPLICANT: Guo, Honliang
; APPLICANT: Aiyeppa, Ashok
; APPLICANT: Lawton, Robert
; TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and
; TITLE OF INVENTION: for Making and Using Them
; FILE REFERENCE: 01-799-A
; CURRENT APPLICATION NUMBER: US/10/327,598
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/344,874
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 1139
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 190
; LENGTH: 32
; TYPE: PRT
; ORGANISM: canis familiaris;
US-10-327-598-190

Query Match 1.3%; Score 7; DB 16; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 GSSATLT 251
DB 12 GSSATLT 18

RESULT 41
US-10-327-598-194
; Sequence 194, Application US/10327598
; Publication No. US20040181039A1
; GENERAL INFORMATION:
; APPLICANT: Krah, Eugene
; APPLICANT: Guo, Honliang
; APPLICANT: Aiyeppa, Ashok
; APPLICANT: Lawton, Robert
; TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and
; TITLE OF INVENTION: for Making and Using Them
; FILE REFERENCE: 01-799-A
; CURRENT APPLICATION NUMBER: US/10/327,598
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/344,874
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 1139
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 194

LENGTH: 32
TYPE: PRT
ORGANISM: canis familiaris;
US-10-327-598-194

Query Match 1.3%; Score 7; DB 16; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0;

OY 245 GSSATLT 251
DB 12 GSSATLT 18

RESULT 42
US-10-327-598-200
Sequence 200, Application US/10327598
Publication No. US20040181039A1
GENERAL INFORMATION:
APPLICANT: Krah, Eugene
APPLICANT: Guo, Honliang
APPLICANT: Aiyaappa, Ashok
APPLICANT: Lawton, Robert
TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and
FILE REFERENCE: 01-799-A
CURRENT APPLICATION NUMBER: US/10/327,598
PRIOR FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: US 60/344,874
NUMBER OF SEQ ID NOS: 1139
SOFTWARE: PatentIn version 3.0
SEQ ID NO 200
LENGTH: 32
TYPE: PRT
ORGANISM: canis familiaris;
US-10-327-598-200

Query Match 1.3%; Score 7; DB 16; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0;

OY 245 GSSATLT 251
DB 12 GSSATLT 18

RESULT 43
US-10-327-598-301
Sequence 301, Application US/10327598
Publication No. US20040181039A1
GENERAL INFORMATION:
APPLICANT: Krah, Eugene
APPLICANT: Guo, Honliang
APPLICANT: Aiyaappa, Ashok
APPLICANT: Lawton, Robert
TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and
FILE REFERENCE: 01-799-A
CURRENT APPLICATION NUMBER: US/10/327,598
PRIOR FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: US 60/344,874
NUMBER OF SEQ ID NOS: 1139
SOFTWARE: PatentIn version 3.0
SEQ ID NO 301
LENGTH: 32
TYPE: PRT
ORGANISM: canis familiaris;
US-10-327-598-301

Query Match 1.3%; Score 7; DB 16; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 245 GSSATLT 251
DB 12 GSSATLT 18

RESULT 44
US-10-327-598-305
Sequence 305, Application US/10327598
Publication No. US20040181039A1
GENERAL INFORMATION:
APPLICANT: Krah, Eugene
APPLICANT: Guo, Honliang
APPLICANT: Aiyaappa, Ashok
APPLICANT: Lawton, Robert
TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and
FILE REFERENCE: 01-799-A
CURRENT APPLICATION NUMBER: US/10/327,598
PRIOR FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: US 60/344,874
NUMBER OF SEQ ID NOS: 1139
SOFTWARE: PatentIn version 3.0
SEQ ID NO 305
LENGTH: 32
TYPE: PRT
ORGANISM: canis familiaris;
US-10-327-598-305

Query Match 1.3%; Score 7; DB 16; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0;

OY 245 GSSATLT 251
DB 12 GSSATLT 18

RESULT 45
US-10-327-598-307
Sequence 307, Application US/10327598
Publication No. US20040181039A1
GENERAL INFORMATION:
APPLICANT: Krah, Eugene
APPLICANT: Guo, Honliang
APPLICANT: Aiyaappa, Ashok
APPLICANT: Lawton, Robert
TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and
FILE REFERENCE: 01-799-A
CURRENT APPLICATION NUMBER: US/10/327,598
PRIOR FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: US 60/344,874
NUMBER OF SEQ ID NOS: 1139
SOFTWARE: PatentIn version 3.0
SEQ ID NO 307
LENGTH: 32
TYPE: PRT
ORGANISM: canis familiaris;
US-10-327-598-307

Query Match 1.3%; Score 7; DB 16; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 245 GSSATLT 251
DB 12 GSSATLT 18

```
RESULT 46
US-10-424-599-184724
; Sequence 184724, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 184724
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_137821C.1.pep
US-10-424-599-184724

Query Match
Best Local Similarity 1.3%; Score 7; DB 15; Length 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 70 SGGDICTL 76
Db 1 SGGDICTL 7

RESULT 47
US-10-424-599-248433
; Sequence 248433, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 248433
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_66365C.1.pep
US-10-424-599-248433

Query Match
Best Local Similarity 1.3%; Score 7; DB 15; Length 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 LRLSLC 36
Db 29 LRLSLC 35

RESULT 48
US-10-097-065-226
; Sequence 226, Application US/10097065
; Publication No. US20030055236A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Paul A. et al.
; TITLE OF INVENTION: 110 Human Secreted Proteins
; FILE REFERENCE: P2021P1
; CURRENT APPLICATION NUMBER: US/10/097,065
```

```
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: PCT/US98/27059
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: 60/070,923
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,007
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,057
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,006
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,369
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,367
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,169
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,053
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,064
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,054
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,008
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,365
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 226
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (59)
; OTHER INFORMATION: Xaa equals stop translation
US-10-097-065-226

Query Match
Best Local Similarity 1.3%; Score 7; DB 14; Length 59;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 323 ALNLPDV 329
Db 43 ALNLPDV 49

RESULT 49
US-10-372-876-226
; Sequence 226, Application US/10372876
; Publication No. US20030204071A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Paul A. et al.
; TITLE OF INVENTION: 110 Human Secreted Proteins
; FILE REFERENCE: P2021P1
; CURRENT APPLICATION NUMBER: US/10/372,876
; CURRENT FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: 09/334,595
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: PCT/US98/27059
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: 60/070,923
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,007
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,057
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,006
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,369
```

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; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,367
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,169
; PRIOR FILING DATE: 1997-12-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 226
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (59)
; OTHER INFORMATION: Xaa equals stop translation
US-10-372-876-226
```

```
Query Match          1.3%; Score 7; DB 14; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      323 ALNLPDV 329
        |||||
Db       43 ALNLPDV 49
```

```

RESULT 50
US-10-437-963-115025
; Sequence 115025, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yinhua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; PRIOR FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 115025
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_18660C.1.pep
US-10-437-963-115025
```

```
Query Match          1.3%; Score 7; DB 16; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      508 RPSRGRP 514
        |||||
Db       21 RPSRGRP 27
```

```

RESULT 51
US-10-125-258-76
; Sequence 76, Application US/10125258
; Publication No. US20030028920A1
; GENERAL INFORMATION:
; APPLICANT: Altier, Daniel J.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert L.
```

```

; APPLICANT: McCutchen, Billy F.
; APPLICANT: Presnall, James K.
; APPLICANT: Weaver, Janine L.
; APPLICANT: Wong, James F. H.
; TITLE OF INVENTION: Antimicrobial Polypeptides and Their
; FILE REFERENCE: 35718/246215
; CURRENT APPLICATION NUMBER: US/10/125,258
; CURRENT FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: 60/285,355
; PRIOR FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 76
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Manduca sexta
US-10-125-258-76
```

```
Query Match          1.3%; Score 7; DB 14; Length 63;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      352 VLISNAV 358
        |||||
Db       14 VLISNAV 20
```

```

RESULT 52
US-10-125-258-77
; Sequence 77, Application US/10125258
; Publication No. US20030028920A1
; GENERAL INFORMATION:
; APPLICANT: Altier, Daniel J.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert L.
; APPLICANT: McCutchen, Billy F.
; APPLICANT: Presnall, James K.
; APPLICANT: Weaver, Janine L.
; APPLICANT: Wong, James F. H.
; TITLE OF INVENTION: Antimicrobial Polypeptides and Their
; FILE REFERENCE: 35718/246215
; CURRENT APPLICATION NUMBER: US/10/125,258
; CURRENT FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: 60/285,355
; PRIOR FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 77
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Manduca sexta
US-10-125-258-77
```

```
Query Match          1.3%; Score 7; DB 14; Length 63;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      352 VLISNAV 358
        |||||
Db       14 VLISNAV 20
```

```

RESULT 53
US-09-764-891-4887
; Sequence 4887, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
```

;; CURRENT FILING DATE: 2001-01-17
;; Prior application data removed - consult PALM or file wrapper
;; NUMBER OF SEQ ID NOS: 10231
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 4887
;; LENGTH: 65
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-764-891-4887

Query Match 1.3%; Score 7; DB 10; Length 65;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 EVPEPTEP 21
|||
Db 56 EVPEPTEP 62

RESULT 54
US-10-424-599-216169
; Sequence 216169, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 216169
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_3722C.1.pep
US-10-424-599-216169

Query Match 1.3%; Score 7; DB 15; Length 65;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 312 LVYPLLA 318
|||||
Db 52 LVYPLLA 58

RESULT 55
US-10-425-115-280879
; Sequence 280879, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 280879
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_19263C.1.pep
US-10-425-115-280879

Query Match 1.3%; Score 7; DB 17; Length 65;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 434 PPSSRLP 440
|||||
Db 33 PPSSRLP 39

RESULT 56
US-10-424-599-227458
; Sequence 227458, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 227458
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_47423C.1.pep
US-10-424-599-227458

Query Match 1.3%; Score 7; DB 15; Length 68;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 GDLICHI 77
|||||
Db 52 GDLICHI 58

RESULT 57
US-10-425-115-299912
; Sequence 299912, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 299912
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(69)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_36591C.1.pep
US-10-425-115-299912

Query Match 1.3%; Score 7; DB 17; Length 69;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 137 DSMIGPS 143

Db 63 DSMIGPS 69

RESULT 58

US-10-437-963-138148
; Sequence 138148, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Bouharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 138148
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_39563C.1.pcp
US-10-437-963-138148

Query Match 1.3%; Score 7; DB 16; Length 72;

Best Local Similarity 100.0%; Pred. No. 3.2e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 102 EOPSLAT 108

Db 32 EOPSLAT 38

RESULT 59

US-10-425-115-198221
; Sequence 198221, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 198221
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_112356C.1.pcp
US-10-425-115-198221

Query Match 1.3%; Score 7; DB 17; Length 72;

Best Local Similarity 100.0%; Pred. No. 3.2e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 303 KLSRLFK 309

Db 55 KLSRLFK 61

RESULT 60

US-10-767-701-38388
; Sequence 38388, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT FILING DATE: 2004-01-23
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 38388
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBT-28MAY03-C57312_1.pcp
US-10-767-701-38388

Query Match 1.3%; Score 7; DB 16; Length 75;

Best Local Similarity 100.0%; Pred. No. 3.3e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 54 DPLTGDE 60

Db 2 DPLTGDE 8

RESULT 61

US-10-424-599-284592
; Sequence 284592, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 284592
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_99011C.1.pcp
US-10-424-599-284592

Query Match 1.3%; Score 7; DB 15; Length 76;

Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 89 SSTDESH 95

Db 49 SSTDESH 55

RESULT 62

US-10-425-115-192652
; Sequence 192652, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

;; TITLE OF INVENTION: Plants
;; FILE REFERENCE: 38-21(53222)B
;; CURRENT APPLICATION NUMBER: US/10/425,115
;; CURRENT FILING DATE: 2003-04-28
;; NUMBER OF SEQ ID NOS: 369326
;; SEQ ID NO 192652
;; LENGTH: 78
;; TYPE: PRT
;; ORGANISM: Zea mays
;; FEATURE:
;; OTHER INFORMATION: Clone ID: MRT4577_107282C.1.pep
US-10-425-115-192652

Query Match 1.3%; Score 7; DB 17; Length 78;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0;

Qy 105 SLATSSN 111
Db 42 SLATSSN 48

RESULT 63
US-10-425-115-305666
; Sequence 305666, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 305666
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_41835C.1.pep
US-10-425-115-305666

Query Match 1.3%; Score 7; DB 17; Length 81;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0;

Qy 1 MRLRVRL 7
Db 10 MRLRVRL 16

RESULT 64
US-10-424-599-167388
; Sequence 167388, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285584
; SEQ ID NO 167388
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Glycine max

;; FEATURE:
;; OTHER INFORMATION: Clone ID: PAT_MRT3847_122169C.1.pep
US-10-424-599-167388
Query Match 1.3%; Score 7; DB 15; Length 83;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0;

Qy 462 SSLRPGP 468
Db 34 SSLRPGP 40

RESULT 65
US-10-437-963-200420
; Sequence 200420, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Bardazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 200420
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_95891C.1.pep
US-10-437-963-200420

Query Match 1.3%; Score 7; DB 16; Length 83;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0;

Qy 496 PGRGCPN 502
Db 11 PGRGCPN 17

RESULT 66
US-10-425-115-363121
; Sequence 363121, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 363121
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_94340C.1.pep
US-10-425-115-363121
Query Match 1.3%; Score 7; DB 17; Length 84;

Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 269 NEIRSVK 275
|||||
Db 8 NEIRSVK 14

RESULT 67
US-10-437-963-174548
Sequence 174548, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovacic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 174548
LENGTH: 85
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_72478C.1.pcp
US-10-437-963-174548

Query Match 1.3%; Score 7; DB 16; Length 85;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 350 RSVLSLS 356
|||||
Db 76 RSVLSLS 82

RESULT 68
US-10-425-115-313746
Sequence 313746, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovacic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 313746
LENGTH: 86
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_49196C.1.pcp
US-10-425-115-313746

Query Match 1.3%; Score 7; DB 17; Length 86;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 HURLSL 35
|||||

Db 75 HURLSL 81

RESULT 69
US-09-864-761-38560
Sequence 38560, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecmca-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annotmax Sequence Listing Engine vers. 1.1
SEQ ID NO 38560
LENGTH: 89
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC004217.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 6.4
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 7.3
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 5.8
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.9
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6.4
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.8
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 6.4
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 6.6
OTHER INFORMATION: SWISSPROT HIT: P47819, EVALUATE 7.40e-01
US-09-864-761-38560

Query Match 1.3%; Score 7; DB 9; Length 89;

Best Local Similarity 100.0%; Pred. No. 3.8e+02; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 58 GDEETLA 64
Db 42 GDEETLA 48

RESULT 70
US-10-424-599-233924
; Sequence 233924, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 233924
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(89)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_53258C.1.pcp
US-10-424-599-233924

Query Match 1.3%; Score 7; DB 15; Length 89;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 329 VEGLVVL 335
Db 12 VEGLVVL 18

RESULT 71
US-10-437-963-154952
; Sequence 154952, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Mu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 154952
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_54763C.1.pcp
US-10-437-963-154952

Query Match 1.3%; Score 7; DB 16; Length 89;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 512 GRPTDGR 518
Db 73 GRPTDGR 79

RESULT 72
US-10-029-386-34281
; Sequence 34281, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 34281
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR19.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.6
; OTHER INFORMATION: SWISSPROT HIT: P53100, EVALUE 7.60e+00
US-10-029-386-34281

Query Match 1.3%; Score 7; DB 14; Length 90;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 275 KRLQLLP 281
Db 27 KRLQLLP 33

RESULT 73
US-10-425-115-306931
; Sequence 306931, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 306931
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_42992C.1.pcp
US-10-425-115-306931

Query Match 1.3%; Score 7; DB 17; Length 92;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 104 PSLATSS 110
Db 21 PSLATSS 27

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RESULT 74
US-09-764-860-518
; Sequence 518, Application US/09764860
; Patent No. US20020094953A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC008
; CURRENT APPLICATION NUMBER: US/09/764,860
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult FALM or file wrapper
; NUMBER OF SEQ ID NOS: 1198
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 518
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-860-518

Query Match 1.3%; Score 7; DB 9; Length 93;
Best Local Similarity 100.0%; Pred.No.4e+02;
Matches 7; Conservative 0; Mismatches 0; Gaps 0;

OY 217 TEAKALS 223
Db 75 TEAKALS 81

RESULT 75
US-10-074-095-518
; Sequence 518, Application US/10074095
; Publication No. US20030077704A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC008C1
; CURRENT APPLICATION NUMBER: US/10/074,095
; CURRENT FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: 09/764,860
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,757
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/226,868
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/216,647
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,267
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/216,880
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,270
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/251,869
; PRIOR FILING DATE: 2000-12-08

; PRIOR APPLICATION NUMBER: 60/235,834
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/234,274
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/234,223
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/228,924
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/224,518
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,369
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/224,519
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,964
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/241,809
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/249,299
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/236,327
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/241,785
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/244,617
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 60/225,268
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,368
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/251,856
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/251,868
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; PRIOR APPLICATION NUMBER: 60/234,997
; PRIOR FILING DATE: 2000-09-25
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; PRIOR APPLICATION NUMBER: 60/229,287
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,513
; PRIOR FILING DATE: 2000-09-05
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; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/229,509
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/236,367
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; PRIOR APPLICATION NUMBER: 60/237,039
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,038
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; PRIOR APPLICATION NUMBER: 60/236,370
; PRIOR FILING DATE: 2000-09-29
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; PRIOR APPLICATION NUMBER: 60/237,040
; PRIOR FILING DATE: 2000-10-02
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; PRIOR APPLICATION NUMBER: 60/246,474

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PRIOR FILING DATE: 2000-09-14

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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,826
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,786
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,221
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/246,475
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/231,243
PRIOR FILING DATE: 2000-09-08

Query Match 1.3%; Score 7; DB 14; Length 93;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 TEAKALS 223
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DB 75 TEAKALS 81

Search completed: November 16, 2004, 07:34:52
Job time : 144 secs

Tue Nov 16 07:54:44 2004

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Page 1

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OM protein - protein search, using sw model

Run on: November 16, 2004, 07:22:05 ; Search time 40 Seconds
(without alignments)
865.450 Million cell updates/sec

Title: US-09-927-458-2

Perfect score: 522
Sequence: 1 MRLRVLKRTWPLEVPEPE.....DRPPPPRSRPTDGRLSFM 522

Scoring table: OLIGO
Gapop 60.0 , Gapext 50.0

Searched: 478139 seqs, 66318000 residues

Word size : 0

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database :

- 1: /cgn2_6/prodata/1/aa/5A_COMB.pep.*
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- 3: /cgn2_6/prodata/1/aa/6A_COMB.pep.*
- 4: /cgn2_6/prodata/1/aa/6B_COMB.pep.*
- 5: /cgn2_6/prodata/1/aa/PCTUS_COMB.pep.*
- 6: /cgn2_6/prodata/1/aa/backfillsl.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	389	74.5	522	4 US-09-591-694-10	Sequence 10, App1
2	330	63.2	443	4 US-09-591-694-8	Sequence 8, App1
3	86	16.5	102	4 US-09-621-976-5935	Sequence 5935, Ap
4	86	16.5	482	4 US-09-385-219A-14	Sequence 14, App1
5	39	7.5	39	4 US-09-385-219A-21	Sequence 21, App1
6	38	7.3	38	3 US-09-172-841-47	Sequence 47, App1
7	38	7.3	38	4 US-09-951-621-47	Sequence 47, App1
8	15	2.9	38	3 US-09-172-841-49	Sequence 49, App1
9	15	2.9	38	4 US-08-951-621-49	Sequence 49, App1
10	8	1.5	304	4 US-09-248-796A-20160	Sequence 20160, A
11	8	1.5	534	4 US-09-270-767-43905	Sequence 43905, A
12	7	1.3	20	2 US-08-484-530-38	Sequence 38, App1
13	7	1.3	20	2 US-08-827-618A-38	Sequence 38, App1
14	7	1.3	20	3 US-08-483-952A-38	Sequence 38, App1
15	7	1.3	20	4 US-08-476-501-38	Sequence 38, App1
16	7	1.3	25	1 US-08-476-501-38	Sequence 38, App1
17	7	1.3	59	4 US-07-792-259-3	Sequence 268, App
18	7	1.3	63	4 US-09-311-021-268	Sequence 268, App
19	7	1.3	63	4 US-09-248-796A-25619	Sequence 25619, A
20	7	1.3	83	4 US-09-513-999C-7211	Sequence 7211, Ap
21	7	1.3	132	2 US-08-647-960-11	Sequence 11, App1
22	7	1.3	136	4 US-09-252-991A-20401	Sequence 20401, A
23	7	1.3	144	4 US-09-252-991A-19404	Sequence 19404, A
24	7	1.3	167	4 US-08-270-767-321A1	Sequence 321A1, A
25	7	1.3	167	4 US-09-270-767-47338	Sequence 47338, A
26	7	1.3	174	4 US-09-746-801A-43	Sequence 43, App1
27	7	1.3	230	4 US-09-333-809-223	Sequence 223, App
27	7	1.3	230	4 US-09-333-809-228	Sequence 228, App

28	7	1.3	230	4 US-09-746-311B-372	Sequence 372, App
29	7	1.3	230	4 US-09-746-311B-377	Sequence 377, App
30	7	1.3	244	2 US-08-933-750C-23	Sequence 23, App1
31	7	1.3	244	3 US-09-234-613-23	Sequence 23, App1
32	7	1.3	283	4 US-09-270-767-42559	Sequence 42559, A
33	7	1.3	285	4 US-10-101-464A-692	Sequence 692, App
34	7	1.3	290	4 US-09-252-991A-27484	Sequence 27484, A
35	7	1.3	292	4 US-09-724-623-91	Sequence 81, App1
36	7	1.3	293	4 US-09-252-991A-25548	Sequence 25548, A
37	7	1.3	315	4 US-09-326-402C-17	Sequence 17, App1
38	7	1.3	316	2 US-08-647-960-2	Sequence 2, App1
39	7	1.3	316	2 US-08-647-960-2	Sequence 2, App1
40	7	1.3	316	3 US-08-946-914-15	Sequence 15, App1
41	7	1.3	316	3 US-08-946-914-17	Sequence 15, App1
42	7	1.3	316	3 US-09-212-146-3	Sequence 15, App1
43	7	1.3	316	4 US-09-656-450-15	Sequence 15, App1
44	7	1.3	316	4 US-09-656-450-17	Sequence 17, App1
45	7	1.3	316	4 US-09-326-402C-9	Sequence 9, App1
46	7	1.3	318	4 US-09-252-991A-20523	Sequence 20523, A
47	7	1.3	325	4 US-09-270-767-43002	Sequence 43002, A
48	7	1.3	328	4 US-10-101-464A-534	Sequence 34, App
49	7	1.3	342	2 US-08-483-151-2	Sequence 2, App1
50	7	1.3	343	2 US-08-624-545-1	Sequence 1, App1
51	7	1.3	343	2 US-09-235-716-1	Sequence 1, App1
52	7	1.3	344	3 US-09-024-532-4	Sequence 4, App1
53	7	1.3	344	4 US-09-705-185-4	Sequence 4, App1
54	7	1.3	345	4 US-07-792-259-12	Sequence 12, App1
55	7	1.3	353	3 US-08-997-803-14	Sequence 14, App1
56	7	1.3	363	1 US-08-458-023B-6	Sequence 6, App1
57	7	1.3	364	1 US-07-792-259-17	Sequence 17, App1
58	7	1.3	383	4 US-09-270-767-39038	Sequence 39038, A
59	7	1.3	383	4 US-09-270-767-49255	Sequence 5455, A
60	7	1.3	386	4 US-10-101-464A-902	Sequence 902, App
61	7	1.3	393	4 US-09-784-077-2	Sequence 2, App1
62	7	1.3	400	4 US-08-845-381E-63	Sequence 63, App1
63	7	1.3	401	3 US-08-289-222E-3	Sequence 3, App1
64	7	1.3	401	3 US-09-054-526B-3	Sequence 3, App1
65	7	1.3	434	3 US-09-516-143A-2	Sequence 2, App1
66	7	1.3	434	4 US-09-964-205-2	Sequence 2, App1
67	7	1.3	435	2 US-08-331-515A-2	Sequence 2, App1
68	7	1.3	435	3 US-09-168-406A-2	Sequence 2, App1
69	7	1.3	460	3 US-09-196-452A-7	Sequence 7, App1
70	7	1.3	468	4 US-09-351-150A-9	Sequence 9, App1
71	7	1.3	476	4 US-09-252-991A-24392	Sequence 24392, A
72	7	1.3	477	4 US-09-134-000C-5553	Sequence 5553, Ap
73	7	1.3	481	4 US-09-252-991A-23317	Sequence 23317, A
74	7	1.3	495	1 US-08-455-559-10	Sequence 10, App1
75	7	1.3	495	1 US-09-145-060-0	Sequence 10, App1
76	7	1.3	495	5 PCT-US94-00657-10	Sequence 10, App1
77	7	1.3	501	2 US-08-288-508C-2	Sequence 2, App1
78	7	1.3	501	4 US-08-981-490B-1	Sequence 1, App1
79	7	1.3	501	4 US-09-386-450D-2	Sequence 2, App1
80	7	1.3	501	4 US-08-920-996A-12	Sequence 12, App1
81	7	1.3	515	3 US-09-134-001C-3565	Sequence 3565, Ap
82	7	1.3	543	3 US-08-161-290-1	Sequence 1, App1
83	7	1.3	584	1 US-08-450-755-1	Sequence 1, App1
84	7	1.3	584	2 US-08-111-907-2	Sequence 2, App1
85	7	1.3	585	1 US-08-485-718-11	Sequence 11, App1
86	7	1.3	585	1 US-08-485-718-13	Sequence 13, App1
87	7	1.3	585	1 US-08-484-530-57	Sequence 57, App1
88	7	1.3	585	2 US-08-484-530-57	Sequence 57, App1
89	7	1.3	585	2 US-08-484-530-59	Sequence 59, App1
90	7	1.3	585	2 US-08-494-624-2	Sequence 2, App1
91	7	1.3	585	2 US-08-827-618A-57	Sequence 57, App1
92	7	1.3	585	2 US-08-827-618A-59	Sequence 59, App1
93	7	1.3	585	3 US-08-483-952A-57	Sequence 57, App1
94	7	1.3	585	3 US-08-483-952A-59	Sequence 59, App1
95	7	1.3	585	3 US-08-451-040-2	Sequence 2, App1
96	7	1.3	585	3 US-09-043-930-3	Sequence 3, App1
97	7	1.3	585	3 US-09-043-930-4	Sequence 4, App1
98	7	1.3	585	3 US-09-043-930-5	Sequence 5, App1
99	7	1.3	585	3 US-09-043-930-6	Sequence 6, App1
100	7	1.3	585	3 US-09-043-930-7	Sequence 7, App1

ALIGNMENTS

RESULT 1

US-05591-694-10
Sequence 10, Application US/09591694
Patent No. 6638734
GENERAL INFORMATION:
APPLICANT: John C. Reed
APPLICANT: Shu-ichi Matsuzawa
TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved
TITLE OF INVENTION: in Protein Degradation, Products and Methods Related Thereto
FILE REFERENCE: P-LJ 4220
CURRENT APPLICATION NUMBER: US/09/591,694
CURRENT FILING DATE: 2000-06-09
EARLIER APPLICATION NUMBER: US 09/330,517
EARLIER FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 522
TYPE: PRT
ORGANISM: Homo sapien
US-09-591-694-10

Query Match 74.5%; Score 389; DB 4; Length 522;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 489; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	33	SILCTWGYSSNTRETTITLYNDPLTCDEBTLASIGVSDILICILLODDIPAPNIPESST	92
DB	33	SILCTWGYSSNTRETTITLYNDPLTCDEBTLASIGVSDILICILLODDIPAPNIPESST	92
QY	93	SEHSSLQNNQPSLATSSNOTSMODEQPSDSFGQAAQSGVWDDSMLGSSQNFASIQ	152
DB	93	SEHSSLQNNQPSLATSSNOTSMODEQPSDSFGQAAQSGVWDDSMLGSSQNFASIQ	152
QY	153	DNAHMAEGTGYPSBPMKLCSESVGQVPHSLLETLYGADCSANDALIVLHLMLESGY	212
DB	153	DNAHMAEGTGYPSBPMKLCSESVGQVPHSLLETLYGADCSANDALIVLHLMLESGY	212
QY	213	IPQGTAKALSMPEKMKLSGVYKLYQVHPLCEGSSATLTCVPLGNLIVNAATLKINNEIR	272
DB	213	IPQGTAKALSMPEKMKLSGVYKLYQVHPLCEGSSATLTCVPLGNLIVNAATLKINNEIR	272
QY	273	SVKRLQILPESFICEKXGENVANTYKDLOKLSLFDQOLVYPLATFROALNLPVFG	332
DB	273	SVKRLQILPESFICEKXGENVANTYKDLOKLSLFDQOLVYPLATFROALNLPVFG	332
QY	333	VVLPLELKLRIFFRLDVRVSLSAVCRDLFTASNDPLMRFYLIRDFRNTYRVQDTW	392
DB	333	VVLPLELKLRIFFRLDVRVSLSAVCRDLFTASNDPLMRFYLIRDFRNTYRVQDTW	392
QY	393	KELYRKRIHQKESPKGRFVWLIPSSSTHTTIFYPNPPLHPPFPSSRLPPGIIIGEYDQR	452
DB	393	KELYRKRIHQKESPKGRFVWLIPSSSTHTTIFYPNPPLHPPFPSSRLPPGIIIGEYDQR	452
QY	453	TLFVVGDPISLILGPGETPSQFPPLRPFRDPVGPLGPNPILPGRGPNDRPFRPSR	512
DB	453	TLFVVGDPISLILGPGETPSQFPPLRPFRDPVGPLGPNPILPGRGPNDRPFRPSR	512
QY	513	RPTDGRLSFM 522	
DB	513	RPTDGRLSFM 522	

RESULT 2
US-05591-694-8
Sequence 8, Application US/09591694
Patent No. 6638734
GENERAL INFORMATION:

APPLICANT: John C. Reed
APPLICANT: Shu-ichi Matsuzawa
TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved
TITLE OF INVENTION: in Protein Degradation, Products and Methods Related Thereto
FILE REFERENCE: P-LJ 4220
CURRENT APPLICATION NUMBER: US/09/591,694
CURRENT FILING DATE: 2000-06-09
EARLIER APPLICATION NUMBER: US 09/330,517
EARLIER FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 443
TYPE: PRT
ORGANISM: Homo sapien
US-09-591-694-8

Query Match 63.2%; Score 330; DB 4; Length 443;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 430; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	92	DEHSSLQNNQPSLATSSNOTSMODEQPSDSFGQAAQSGVWDDSMLGSSQNFASIQ	151
DB	92	DEHSSLQNNQPSLATSSNOTSMODEQPSDSFGQAAQSGVWDDSMLGSSQNFASIQ	151
QY	152	QNAHMAEGTGYPSBPMKLCSESVGQVPHSLLETLYGADCSANDALIVLHLMLESG	211
DB	152	QNAHMAEGTGYPSBPMKLCSESVGQVPHSLLETLYGADCSANDALIVLHLMLESG	211
QY	212	YIPQGTAKALSMPEKMKLSGVYKLYQVHPLCEGSSATLTCVPLGNLIVNAATLKINNEI	271
DB	212	YIPQGTAKALSMPEKMKLSGVYKLYQVHPLCEGSSATLTCVPLGNLIVNAATLKINNEI	271
QY	272	RSVKRLQILPESFICEKXGENVANTYKDLOKLSLFDQOLVYPLATFROALNLPVFG	331
DB	272	RSVKRLQILPESFICEKXGENVANTYKDLOKLSLFDQOLVYPLATFROALNLPVFG	331
QY	332	LVLPLELKLRIFFRLDVRVSLSAVCRDLFTASNDPLMRFYLIRDFRNTYRVQDTW	391
DB	332	LVLPLELKLRIFFRLDVRVSLSAVCRDLFTASNDPLMRFYLIRDFRNTYRVQDTW	391
QY	392	WEELYRKRIHQKESPKGRFVWLIPSSSTHTTIFYPNPPLHPPFPSSRLPPGIIIGEYDQR	451
DB	392	WEELYRKRIHQKESPKGRFVWLIPSSSTHTTIFYPNPPLHPPFPSSRLPPGIIIGEYDQR	451
QY	452	PTLFVVGDPISLILGPGETPSQFPPLRPFRDPVGPLGPNPILPGRGPNDRPFRPSR	511
DB	452	PTLFVVGDPISLILGPGETPSQFPPLRPFRDPVGPLGPNPILPGRGPNDRPFRPSR	511
QY	512	GRPTDGRLSFM 522	
DB	512	GRPTDGRLSFM 522	

RESULT 3
US-05591-694-8
Sequence 8, Application US/09591694
Patent No. 6638734
GENERAL INFORMATION:
APPLICANT: Dumas Mline Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET-054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 5935
LENGTH: 102
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:

Tue Nov 16 07:54:44 2004

us-09-927-458-2.01igo.rat

Page 3

NAME/KEY: UNSURE
LOCATION: 87
OTHER INFORMATION: Xaa = Cys, Gly
US-09-621-976-5935

Query Match 16.5%; Score 86; DB 4; Length 102;
Best Local Similarity 100.0%; Pred. No. 5.2e-78;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 413 MLPPSSHTTFFYPNPLHPPFPSSRLPFGIIGEDDRTLPYVGDPISSLIIPGGETP 472
DB 1 MLPPSSHTTFFYPNPLHPPFPSSRLPFGIIGEDDRTLPYVGDPISSLIIPGGETP 60

QY 473 SCFPPPLRPDPVGPLGPNPILPGR 498
DB 61 SCFPPPLRPDPVGPLGPNPILPGR 86

RESULT 4
US-09-385-219A-14
Sequence 14, Application US/09385219A
Patent No. 6720181
GENERAL INFORMATION:
APPLICANT: Chiatour, D.
APPLICANT: Pagano, M.
APPLICANT: Laties, E.
TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
FILE REFERENCE: 5914-081
CURRENT APPLICATION NUMBER: US/09/385,219A
CURRENT FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: 60/058,355
PRIOR FILING DATE: 1998-08-28
PRIOR APPLICATION NUMBER: 60/118,568
PRIOR FILING DATE: 1999-02-03
PRIOR APPLICATION NUMBER: 60/124,449
PRIOR FILING DATE: 1999-03-15
NUMBER OF SEQ ID NOS: 90
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 482
TYPE: PRT
ORGANISM: Homo sapiens
US-09-385-219A-14

Query Match 16.5%; Score 86; DB 4; Length 482;
Best Local Similarity 100.0%; Pred. No. 2.2e-77;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 202 LCEGSSATLTCVPLGNLIYVNAATKINNEIRSVKRLQLPDESFICEKLGENVANYIKDL 261
QY 302 QKLSRLFKDQVYPLLAFTROALNLP 327
DB 262 QKLSRLFKDQVYPLLAFTROALNLP 287

RESULT 5
US-09-385-219A-21
Sequence 21, Application US/09385219A
Patent No. 6720181
GENERAL INFORMATION:
APPLICANT: Chiatour, D.
APPLICANT: Pagano, M.
APPLICANT: Laties, E.
TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
FILE REFERENCE: 5914-081
CURRENT APPLICATION NUMBER: US/09/385,219A
CURRENT FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: 60/098,355
PRIOR FILING DATE: 1998-08-28
PRIOR APPLICATION NUMBER: 60/118,568
PRIOR FILING DATE: 1999-02-03

PRIOR APPLICATION NUMBER: 60/124,449
PRIOR FILING DATE: 1999-03-15
NUMBER OF SEQ ID NOS: 90
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21
LENGTH: 39
TYPE: PRT
ORGANISM: Homo sapiens
US-09-385-219A-21

Query Match 7.5%; Score 39; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 2.4e-31;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 LPLEKLRIFRLDVRVSLSAVCRDLFTASNDPLMW 373
DB 1 LPLEKLRIFRLDVRVSLSAVCRDLFTASNDPLMW 39

RESULT 6
US-09-172-841-47
Sequence 47, Application US/09172841
Patent No. 6232081
GENERAL INFORMATION:
APPLICANT: Harper, Jeffrey W.
APPLICANT: Elledge, Stephen J.
TITLE OF INVENTION: F-BOX PROTEINS AND GENES
FILE REFERENCE: BCM-03510
CURRENT APPLICATION NUMBER: US/09/172,841
CURRENT FILING DATE: 1998-10-15
EARLIER APPLICATION NUMBER: 08/951,621
EARLIER FILING DATE: 1997-10-16
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 47
LENGTH: 38
TYPE: PRT
ORGANISM: Homo sapiens
US-09-172-841-47

Query Match 7.3%; Score 38; DB 3; Length 38;
Best Local Similarity 100.0%; Pred. No. 2.3e-30;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 LPLEKLRIFRLDVRVSLSAVCRDLFTASNDPLMW 372
DB 1 LPLEKLRIFRLDVRVSLSAVCRDLFTASNDPLMW 38

RESULT 7
US-08-951-621-47
Sequence 47, Application US/08951621
Patent No. 6573094
GENERAL INFORMATION:
APPLICANT: HARPER, JEFFREY W.
APPLICANT: ELLEDGE, STEPHEN J.
TITLE OF INVENTION: F-BOX GENES AND PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medien & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/951,621
FILING DATE: 16-OCT-1997

CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: BCM-02999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-08-951-621-47

Query Match
Best Local Similarity 100.0%; Score 38; DB 4; Length 38;
Pred. No. 2,3e-30;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 335 LPLELKLRIFFRLDVSLSAVCRDIFTSNDPLIM 372
Db 1 LPLELKLRIFFRLDVSLSAVCRDIFTSNDPLIM 38

RESULT 8
US-09-172-841-49
Sequence 49, Application US/09172841
Patent No. 6232081
GENERAL INFORMATION:
APPLICANT: Harper, Jeffrey W.
APPLICANT: Ellsper, Stephen J.
TITLE OF INVENTION: F-BOX PROTEINS AND GENES
FILE REFERENCE: BCM-03510
CURRENT APPLICATION NUMBER: US/09/172,841
CURRENT FILING DATE: 1998-10-15
EARLIER APPLICATION NUMBER: 08/951,621
EARLIER FILING DATE: 1997-10-16
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 49
LENGTH: 38
TYPE: PRT
ORGANISM: Mus musculus
US-09-172-841-49

Query Match
Best Local Similarity 100.0%; Score 15; DB 3; Length 38;
Pred. No. 2,4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 335 LPLELKLRIFFRLDV 349
Db 1 LPLELKLRIFFRLDV 15

RESULT 9
US-08-951-621-49
Sequence 49, Application US/08951621
Patent No. 6573094
GENERAL INFORMATION:
APPLICANT: HARPER, JEFFREY W.
APPLICANT: ELLSPE, STEPHEN J.
TITLE OF INVENTION: F-BOX GENES AND PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medien & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/951,621
FILING DATE: 16-OCT-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: BCM-02999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-08-951-621-49

Query Match
Best Local Similarity 100.0%; Score 15; DB 4; Length 38;
Pred. No. 2,4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 335 LPLELKLRIFFRLDV 349
Db 1 LPLELKLRIFFRLDV 15

RESULT 10
US-09-248-796A-20160
Sequence 20160, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 20160
LENGTH: 304
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-20160

Query Match
Best Local Similarity 100.0%; Score 8; DB 4; Length 304;
Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 332 LVVLPLEL 339
Db 22 LVVLPLEL 29

RESULT 11
US-09-270-767-43905
Sequence 43905, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7325-094
CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 43905
LENGTH: 534
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-43905

Query Match 1.5%; Score 8; DB 4; Length 534;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 TRFTITLN 51
Db 98 TRFTITLN 105

RESULT 12
US-08-484-530-38
Sequence 38, Application US/08484530
Patent No. 5846740
GENERAL INFORMATION:
APPLICANT: Tobin, Allan J
APPLICANT: Exlander, Mark G
APPLICANT: Kaufman, Daniel L.
TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,530
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Treacartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-60780-8/RFT/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-530-38

Query Match 1.3%; Score 7; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 227 KWKLSGV 233
Db 9 KWKLSGV 15

RESULT 13
US-08-827-618A-38

Sequence 38, Application US/08827618A
Patent No. 5998366
GENERAL INFORMATION:
APPLICANT: Tobin, Allan J
APPLICANT: Exlander, Mark G
APPLICANT: Kaufman, Daniel L.
TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,618A
FILING DATE: 09-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,725
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/716,909
FILING DATE: 18-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/586,536
FILING DATE: 21-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Treacartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-60780-12/RFT/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-827-618A-38

Query Match 1.3%; Score 7; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 227 KWKLSGV 233
Db 9 KWKLSGV 15

RESULT 14
US-08-483-952A-38
Sequence 38, Application US/08483952A
Patent No. 6011139
GENERAL INFORMATION:
APPLICANT: Tobin, Allan J
APPLICANT: Exlander, Mark G
APPLICANT: Kaufman, Daniel L.
TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA

COUNTRY: US
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,952A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,859
FILING DATE: 17-SEP-1993
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/716,909
FILING DATE: 18-JUN-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/586,536
FILING DATE: 21-SEP-1990
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Treccarlin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-60780-7/RPT/NTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-483-952A-38

Query Match 1.3%; Score 7; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 227 KWKLSGV 233
|||||
9 KWKLSGV 15

Db 9 KWKLSGV 15

RESULT 15
US-08-476-501-38
Sequence 38, Application US/08476501
Patent No. 6455267
GENERAL INFORMATION:
APPLICANT: TOBIN, Allan J.
APPLICANT: ERLANDER, Mark G.
APPLICANT: KAUFMAN, Daniel L.
TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Teat, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,501
FILING DATE: 07-JUN-1995

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertam I.
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: A60780-10/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-476-501-38

Query Match 1.3%; Score 7; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 227 KWKLSGV 233
|||||
9 KWKLSGV 15

Db 9 KWKLSGV 15

RESULT 16
US-07-792-259-3
Sequence 3, Application US/07792259
Patent No. 5286638
GENERAL INFORMATION:
APPLICANT: TANAKA, YOSHIKAZU
APPLICANT: ASHIZAKI, TOSHIHIKO
APPLICANT: HATANAKA, HARUO
APPLICANT: SHIBANO, YUJI
APPLICANT: AMACHI, TERUO
APPLICANT: NAKAYAMA, TORU
APPLICANT: SUMIDA, MOTOO
TITLE OF INVENTION: PEROXIDE GENE OF MICROBIAL ORIGIN
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1615 L. STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/792,259
FILING DATE: 19911115
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26581
REFERENCE/DOCKET NUMBER: 9437/93433
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3067
TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-792-259-3

Query Match 1.3%; Score 7; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 463 SLIPGPG 469
|||||
Db 10 SLIPGPG 16

RESULT 17

US-09-311-021-268
; Sequence 268, Application US/09311021
; Patent No. 6706869
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI 6300-11A
; CURRENT APPLICATION NUMBER: US/09/311,021
; CURRENT FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 268
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-311-021-268

Query Match 1.3%; Score 7; DB 4; Length 59;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 466 PGPGETP 472
|||||
Db 27 PGPGETP 33

RESULT 18
US-09-248-796A-25619
; Sequence 25619, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 25619
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-25619

Query Match 1.3%; Score 7; DB 4; Length 63;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 ICLILQD 80
|||||
Db 19 ICLILQD 25

RESULT 19
US-09-513-999C-7211

; Sequence 7211, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, G.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59, US2, REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 7211
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Homo sapiens

; NAME/KEY: UNSURE
; LOCATION: 12
; OTHER INFORMATION: Xaa=Arg or Thr
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 29
; OTHER INFORMATION: Xaa=Arg or Ser
US-09-513-999C-7211

Query Match 1.3%; Score 7; DB 4; Length 83;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 275 KRLQILP 281
|||||
Db 21 KRLQILP 27

RESULT 20
US-08-647-960-11
; Sequence 11, Application US/08647960
; Patent No. 5908761
; GENERAL INFORMATION:
; APPLICANT: ZICK, Yehiel
; TITLE OF INVENTION: GALECTIN-8 AND GALECTIN-8-LIKE PROTEINS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/647,960
; FILING DATE: 30-MAY-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 107880
; FILING DATE: 05-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: ZICK=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3527
; INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:
 LENGTH: 132 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-647-960-11

Query Match 1.3%; Score 7; DB 2; Length 132;
 Best Local Similarity 100.0%; Pred. No. 78;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 345 RLIDVRS 351
 Db 125 RLIDVRS 131

RESULT 21
 US-09-252-991A-20401
 ; Sequence 20401, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 20401
 ; LENGTH: 136
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-20401

Query Match 1.3%; Score 7; DB 4; Length 136;
 Best Local Similarity 100.0%; Pred. No. 80;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 213 IPQTEA 219
 Db 79 IPQTEA 85

RESULT 22
 US-09-252-991A-19404
 ; Sequence 19404, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 19404
 ; LENGTH: 144
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-19404

Query Match 1.3%; Score 7; DB 4; Length 144;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 108 TSSNOTS 114
 Db 130 TSSNOTS 136

RESULT 23
 US-09-270-767-32121
 ; Sequence 32121, Application US/09270767
 ; Patent No. 6703491
 ; GENERAL INFORMATION:
 ; APPLICANT: Homburger et al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
 ; FILE REFERENCE: File Reference: 7326-094
 ; CURRENT APPLICATION NUMBER: US/09/270,767
 ; CURRENT FILING DATE: 1999-03-17
 ; NUMBER OF SEQ ID NOS: 62517
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 32121
 ; LENGTH: 167
 ; TYPE: PRT
 ; ORGANISM: *Drosophila melanogaster*
 US-09-270-767-32121

Query Match 1.3%; Score 7; DB 4; Length 167;
 Best Local Similarity 100.0%; Pred. No. 97;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 468 PGETPSQ 474
 Db 48 PGETPSQ 54

RESULT 24
 US-09-270-767-47338
 ; Sequence 47338, Application US/09270767
 ; Patent No. 6703491
 ; GENERAL INFORMATION:
 ; APPLICANT: Homburger et al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
 ; FILE REFERENCE: File Reference: 7326-094
 ; CURRENT APPLICATION NUMBER: US/09/270,767
 ; CURRENT FILING DATE: 1999-03-17
 ; NUMBER OF SEQ ID NOS: 62517
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 47338
 ; LENGTH: 167
 ; TYPE: PRT
 ; ORGANISM: *Drosophila melanogaster*
 US-09-270-767-47338

Query Match 1.3%; Score 7; DB 4; Length 167;
 Best Local Similarity 100.0%; Pred. No. 97;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 468 PGETPSQ 474
 Db 48 PGETPSQ 54

RESULT 25
 US-09-746-801A-43
 ; Sequence 43, Application US/09746801A
 ; Patent No. 6689940
 ; GENERAL INFORMATION:
 ; APPLICANT: Wagner, et al.
 ; TITLE OF INVENTION: GENES REGULATING CIRCADIAN CLOCK FUNCTION AND PHOTOPERIODISM
 ; FILE REFERENCE: 1505-54357
 ; CURRENT APPLICATION NUMBER: US/09/746,801A
 ; CURRENT FILING DATE: 2000-12-20
 ; NUMBER OF SEQ ID NOS: 68
 ; SOFTWARE: Patent Version 3.1
 ; SEQ ID NO 43

LENGTH: 174
TYPE: PRT
ORGANISM: Pism sativum
US-09-746-801A-43

Query Match 1.3%; Score 7; DB 4; Length 174;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 VPHSLER 185
Db 159 VPHSLER 165

RESULT 26
US-09-333-809-223
Sequence 223, Application US/09333809
Patent No. 6667175
GENERAL INFORMATION:
APPLICANT: Suciu-Foca, Nicole
TITLE OF INVENTION: GENERATION OF ANTIGEN SPECIFIC T SUPPRESSOR CELLS FOR TREATMENT
FILE REFERENCE: 0575/58332
CURRENT APPLICATION NUMBER: US/09/333,809
CURRENT FILING DATE: 2003-01-14
NUMBER OF SEQ ID NOS: 229
SOFTWARE: PatentIn version 3.1
SEQ ID NO 223
LENGTH: 230
TYPE: PRT
ORGANISM: swine
US-09-333-809-223

Query Match 1.3%; Score 7; DB 4; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 EHSSLON 100
Db 177 EHSSLON 183

RESULT 27
US-09-333-809-228
Sequence 228, Application US/09333809
Patent No. 6667175
GENERAL INFORMATION:
APPLICANT: Suciu-Foca, Nicole
TITLE OF INVENTION: GENERATION OF ANTIGEN SPECIFIC T SUPPRESSOR CELLS FOR TREATMENT
FILE REFERENCE: 0575/58332
CURRENT APPLICATION NUMBER: US/09/333,809
CURRENT FILING DATE: 2003-01-14
NUMBER OF SEQ ID NOS: 229
SOFTWARE: PatentIn version 3.1
SEQ ID NO 228
LENGTH: 230
TYPE: PRT
ORGANISM: swine
US-09-333-809-228

Query Match 1.3%; Score 7; DB 4; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 EHSSLON 100
Db 177 EHSSLON 183

RESULT 28
US-09-746-311B-372
Sequence 372, Application US/09746311B

Patent No. 6759239
GENERAL INFORMATION:
APPLICANT: Suciu-Foca, Nicole
APPLICANT: Liu, Zhuro
APPLICANT: Chang, Chih-Chao
APPLICANT: Cortesini, Raffaello
TITLE OF INVENTION: Generation of Antigen-Specific T Suppressor Cells For Treatment of
FILE REFERENCE: 0575/58332-B
CURRENT APPLICATION NUMBER: US/09/746,311B
CURRENT FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: PCT/US00/16594
NUMBER OF SEQ ID NOS: 382
SOFTWARE: PatentIn version 3.1
SEQ ID NO 372
LENGTH: 230
TYPE: PRT
ORGANISM: Swine SLA-DOB
US-09-746-311B-372

Query Match 1.3%; Score 7; DB 4; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 EHSSLON 100
Db 177 EHSSLON 183

RESULT 29
US-09-746-311B-377
Sequence 377, Application US/09746311B
Patent No. 6759239
GENERAL INFORMATION:
APPLICANT: Suciu-Foca, Nicole
APPLICANT: Liu, Zhuro
APPLICANT: Chang, Chih-Chao
APPLICANT: Cortesini, Raffaello
TITLE OF INVENTION: Generation of Antigen-Specific T Suppressor Cells For Treatment of
FILE REFERENCE: 0575/58332-B
CURRENT APPLICATION NUMBER: US/09/746,311B
CURRENT FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: PCT/US00/16594
NUMBER OF SEQ ID NOS: 382
SOFTWARE: PatentIn version 3.1
SEQ ID NO 377
LENGTH: 230
TYPE: PRT
ORGANISM: Swine SLA-DOB
US-09-746-311B-377

Query Match 1.3%; Score 7; DB 4; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 EHSSLON 100
Db 177 EHSSLON 183

RESULT 30
US-08-933-750C-23
Sequence 23, Application US/08933750C
Patent No. 5932442
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Tanice

APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750C
FILING DATE: September 23, 1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PR-0356 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SPLINOT04
CLONE: 1561587
US-08-933-750C-23

Query Match 1.3%; Score 7; DB 2; Length 244;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 348 DVSYS 354
DB 229 DVSYS 235

RESULT 31
US-09-234-613-23
Sequence 23, Application US/09234613
Patent No. 6132973
GENERAL INFORMATION:
APPLICANT: Tai, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA

ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,613
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750
FILING DATE: September 23, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PR-0356 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SPLINOT04
CLONE: 1561587
US-09-234-613-23

Query Match 1.3%; Score 7; DB 3; Length 244;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 348 DVSYS 354
DB 229 DVSYS 235

RESULT 32
US-09-270-767-42559
Sequence 42559, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-034
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 42559
LENGTH: 283
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-42559

Query Match 1.3%; Score 7; DB 4; Length 283;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 348 DVSYS 354
DB 268 DVSYS 274

RESULT 33
US-10-101-464A-692
Sequence 692, Application US/10101464A
Patent No. 6768041
GENERAL INFORMATION:


```
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020c2
CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: PCT/US00/00724
PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 682
LENGTH: 285
TYPE: PRT
ORGANISM: Pinus radiata
US-10-101-464A-692
```

```
Query Match
Best Local Similarity 1.3%; Score 7; DB 4; Length 285;
Pred. No. 1.6e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;
```

```
QY 351 SVLSLSA 357
DB 88 SVLSLSA 94
```

```
RESULT 34
US-09-252-991A-27484
Sequence 27484, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO: 27484
LENGTH: 290
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27484
```

```
Query Match
Best Local Similarity 1.3%; Score 7; DB 4; Length 290;
Pred. No. 1.6e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;
```

```
QY 466 PGRGPT 472
DB 277 PGRGPT 283
```

```
RESULT 35
US-09-724-623-81
Sequence 81, Application US/09724623
Patent No. 6476209
GENERAL INFORMATION:
APPLICANT: Glenn, Matthew
APPLICANT: Lubbers, Mark W
APPLICANT: Dekker, James
TITLE OF INVENTION: Polynucleotides, materials incorporating
```

```
TITLE OF INVENTION: them, and methods for using them.
FILE REFERENCE: 1048U1
CURRENT APPLICATION NUMBER: US/09/724,623
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 124
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 81
LENGTH: 292
TYPE: PRT
ORGANISM: Lactobacillus rhamnosus
US-09-724-623-81
```

```
Query Match
Best Local Similarity 1.3%; Score 7; DB 4; Length 292;
Pred. No. 1.6e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;
```

```
QY 312 LVYPLLA 318
DB 141 LVYPLLA 147
```

```
RESULT 36
US-09-252-991A-25548
Sequence 25548, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO: 25548
LENGTH: 293
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25548
```

```
Query Match
Best Local Similarity 1.3%; Score 7; DB 4; Length 293;
Pred. No. 1.6e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;
```

```
QY 104 PSLATSS 110
DB 32 PSLATSS 38
```

```
RESULT 37
US-09-326-402C-17
Sequence 17, Application US/09326402C
Patent No. 6759192
GENERAL INFORMATION:
APPLICANT: Blumenfeld, Marta
APPLICANT: Bougueleret, Lydie
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Polymorphic Markers of Prostate Carcinoma Tumor Antigen-1 (PCTA-1)
FILE REFERENCE: GEN-1112X01
CURRENT APPLICATION NUMBER: US/09/326,402C
CURRENT FILING DATE: 1999-06-04
PRIOR APPLICATION NUMBER: 60/088,187
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/102,324
PRIOR FILING DATE: 1998-09-28
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 17
LENGTH: 315
TYPE: PRT
```

ORGANISM: Mus musculus
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1)..(315)
OTHER INFORMATION: amino acid sequence of PCTA.mus
US-09-326-402C-17

Query Match 1.3%; Score 7; DB 4; Length 315;
Best Local Similarity 100.0%; Pred.No.1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 RLLDVS 351
|||||
DB 308 RLLDVS 314

RESULT 38
US-08-728-521-3
Sequence 3, Application US/08728521
Patent No. 5869289
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: HUMAN GALECTIN HOMOLOG
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,521
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0137 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 717032
US-08-728-521-3
Query Match 1.3%; Score 7; DB 2; Length 316;
Best Local Similarity 100.0%; Pred.No.1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 RLLDVS 351
|||||
DB 309 RLLDVS 315

RESULT 39
US-08-647-960-2

Sequence 2, Application US/08647960
Patent No. 5908761
GENERAL INFORMATION:
APPLICANT: Zick, Yehiel
TITLE OF INVENTION: GALECTIN-8 AND GALECTIN-8-LIKE PROTEINS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: BROWDY AND NEWMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/647,960
FILING DATE: 30-MAY-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107880
FILING DATE: 05-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: ZICK=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3527
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-647-960-2

Query Match 1.3%; Score 7; DB 2; Length 316;
Best Local Similarity 100.0%; Pred.No.1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 RLLDVS 351
|||||
DB 309 RLLDVS 315

RESULT 40
US-08-946-914-15
Sequence 15, Application US/08946914
Patent No. 6027916
GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Gentz, Reiner L.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Galectin 8, 9, 10 and 10SV
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Sterne, Kessler, Goldstein, & Fox P.L.L.C.
STREET: 1100 New York Ave., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/946,914

FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,093
FILING DATE: 09-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE//DOCKET NUMBER: 1488.0560001/EKS/SGW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-946-914-15

Query Match 1.3%; Score 7; DB 3; Length 316;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 RLLDVS 351
DB 309 RLLDVS 315

RESULT 41
US-08-946-914-17
Sequence 17, Application US/08946914
Patent No. 6027916
GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Gentz, Reiner L.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Galectin 8, 9, 10 and 10sV
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein, & Fox P.L.L.C.
STREET: 1100 New York Ave., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/946,914
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,093
FILING DATE: 09-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE//DOCKET NUMBER: 1488.0560001/EKS/SGW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: protein

US-08-946-914-17
Query Match 1.3%; Score 7; DB 3; Length 316;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 RLLDVS 351
DB 309 RLLDVS 315

RESULT 42
US-09-212-146-3
Sequence 3, Application US/09212146
Patent No. 6281333
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: HUMAN GALECTIN HOMOLOG
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/212,146
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/728,521
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE//DOCKET NUMBER: PF-0137 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 717032
US-09-212-146-3

Query Match 1.3%; Score 7; DB 3; Length 316;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 RLLDVS 351
DB 309 RLLDVS 315

RESULT 43
US-09-656-450-15
Sequence 15, Application US/09656450
Patent No. 6468768
GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Gentz, Reiner L.

```
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Galactin 9 and 10SV Polynucleotides
; FILE REFERENCE: 1488.0560003
; CURRENT APPLICATION NUMBER: US/09/656,450
; CURRENT FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 09/263,689
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: US 08/946,914
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: US 60/028,093
; PRIOR FILING DATE: 1996-10-09
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Rat
; US-09-656-450-15

Query Match      1.3%; Score 7; DB 4; Length 316;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      345 RLDDVRS 351
      |||||
      |||||
DB      309 RLDDVRS 315

RESULT 44
US-09-656-450-17
; Sequence 17, Application US/09656450
; Patent No. 6468768
; GENERAL INFORMATION:
; APPLICANT: Gentz, Retner L.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Galactin 9 and 10SV Polynucleotides
; FILE REFERENCE: 1488.0560003
; CURRENT APPLICATION NUMBER: US/09/656,450
; CURRENT FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 09/263,689
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: US 08/946,914
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: US 60/028,093
; PRIOR FILING DATE: 1996-10-09
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Rat
; US-09-656-450-17

Query Match      1.3%; Score 7; DB 4; Length 316;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      345 RLDDVRS 351
      |||||
      |||||
DB      309 RLDDVRS 315

RESULT 45
US-09-326-402C-9
; Sequence 9, Application US/09326402C
; Patent No. 6759192
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bousseleret, Lydie
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Polymorphic Markers of Prostate Carcinoma Tumor Antigen-1 (POTA-1
; FILE REFERENCE: GEN-1112XCI
```

```
; CURRENT APPLICATION NUMBER: US/09/326,402C
; CURRENT FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 60/086,187
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/102,324
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-326-402C-9

Query Match      1.3%; Score 7; DB 4; Length 316;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      345 RLDDVRS 351
      |||||
      |||||
DB      309 RLDDVRS 315

RESULT 46
US-09-252-991A-20523
; Sequence 20523, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfeld et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20523
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-20523

Query Match      1.3%; Score 7; DB 4; Length 318;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 RLVRRL 8
      |||||
      |||||
DB      54 RLVRRL 60

RESULT 47
US-09-270-767-43002
; Sequence 43002, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43002
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
; US-09-270-767-43002
```

Query Match 1.3%; Score 7; DB 4; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 334 VLPELTK 340
DB 108 VLPELTK 114

RESULT 48
US-10-101-464A-534
Sequence 534, Application US/10101464A
Patent No. 6768841
GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020c2
CURRENT APPLICATION NUMBER: US/10/101.464A
CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: PCT/US00/00724
PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 534
LENGTH: 328
TYPE: PRT
ORGANISM: Eucalyptus grandis
US-10-101-464A-534

Query Match 1.3%; Score 7; DB 4; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 DEETLAS 65
DB 216 DEETLAS 222

RESULT 49
US-08-483-151-2
Sequence 2, Application US/08483151
Patent No. 5858752
GENERAL INFORMATION:
APPLICANT: Seed, Brian
APPLICANT: Holgersson, Jan
TITLE OF INVENTION: FUCOSYLTRANSFERASE GENES AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483.151
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: Lech, Karen F.
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/278001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 342 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-151-2

Query Match 1.3%; Score 7; DB 2; Length 342;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RVRVRL 8
DB 304 RVRVRL 310

RESULT 50
US-08-624-545-1
Sequence 1, Application US/08624545
Patent No. 5817495
GENERAL INFORMATION:
APPLICANT: Pedersen, Anders
APPLICANT: Vind, Jesper
APPLICANT: Svendsen, Allan
APPLICANT: Cherry, Joel
APPLICANT: Lamsa, Michael
APPLICANT: Schneider, Paule
TITLE OF INVENTION: H2O2-Stable Peroxidase Variants
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58174950 No. 58174950th America
STREET: 405 Lexington Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10174

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/624.545
FILING DATE: 07-MAY-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Agis, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 4072.204
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 867-0123
TELEFAX: (212) 878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 343 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-624-545-1

Query Match 1.3%; Score 7; DB 2; Length 343;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 463 SLIPPG 469
DB 150 SLIPPG 156

RESULT 51
US-09-235-736-1
; Sequence 1, Application US/09235736
; Patent No. 5968883
; GENERAL INFORMATION:
; APPLICANT: Cherry, Joel
; APPLICANT: Svendsen, Allen
; APPLICANT: Damus, Ture
; APPLICANT: Schneider, Palle
; TITLE OF INVENTION: Peroxidase Variants
; FILE REFERENCE: 4938.204-US
; CURRENT APPLICATION NUMBER: US/09/235,736
; EARLIER FILING DATE: 1999-01-22
; EARLIER APPLICATION NUMBER: 0937/96
; EARLIER FILING DATE: 1996-09-03
; EARLIER APPLICATION NUMBER: PCT/DK97/00361
; EARLIER FILING DATE: 1997-09-02
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Coprinus cinereus
US-09-235-736-1

Query Match 1.3%; Score 7; DB 2; Length 343;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 463 SLIPPG 469
DB 150 SLIPPG 156

RESULT 52
US-09-024-532-4
; Sequence 4, Application US/09024532
; Patent No. 6245901
; GENERAL INFORMATION:
; APPLICANT: von der Osten, Claus
; APPLICANT: Olsen, Arne Agerlin
; APPLICANT: Roggen, Erwin Ludo
; TITLE OF INVENTION: A Modified Polypeptide
; FILE REFERENCE: 4923.204-US
; CURRENT APPLICATION NUMBER: US/09/024,532
; EARLIER FILING DATE: 1998-02-17
; EARLIER APPLICATION NUMBER: PCT/DK98/00046
; EARLIER FILING DATE: 1998-02-06
; EARLIER APPLICATION NUMBER: 0135/97
; EARLIER FILING DATE: 1997-02-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Arthromyces ramosus
US-09-024-532-4

Query Match 1.3%; Score 7; DB 3; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 463 SLIPPG 469
DB 151 SLIPPG 157

RESULT 53

US-09-705-185-4
; Sequence 4, Application US/09705185
; Patent No. 6623950
; GENERAL INFORMATION:
; APPLICANT: von der Osten, Claus
; APPLICANT: Olsen, Arne Agerlin
; APPLICANT: Roggen, Erwin Ludo
; TITLE OF INVENTION: A Modified Polypeptide
; FILE REFERENCE: 4923.204-US
; CURRENT APPLICATION NUMBER: US/09/705,185
; EARLIER FILING DATE: 2000-11-02
; EARLIER APPLICATION NUMBER: 09/024,532
; EARLIER FILING DATE: 1998-02-17
; EARLIER APPLICATION NUMBER: PCT/DK98/00046
; EARLIER FILING DATE: 1998-02-06
; EARLIER APPLICATION NUMBER: 0135/97
; EARLIER FILING DATE: 1997-02-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Arthromyces ramosus
US-09-705-185-4

Query Match 1.3%; Score 7; DB 4; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 463 SLIPPG 469
DB 151 SLIPPG 157

RESULT 54
US-07-792-259-12
; Sequence 12, Application US/07792259
; Patent No. 5286638
; GENERAL INFORMATION:
; APPLICANT: TANAKA, YOSHIKAZU
; APPLICANT: ASHIKARI, TOSHIHIKO
; APPLICANT: HATANAKA, HARUO
; APPLICANT: SHIBANO, YUJI
; APPLICANT: AMACHI, TERUO
; APPLICANT: NAKAYAMA, TORU
; APPLICANT: SUMIDA, MOTOO
; TITLE OF INVENTION: PEROXIDE GENE OF MICROBIAL ORIGIN
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1615 L. STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/792,259
; FILING DATE: 19911115
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: SCOTT, WATSON T.
; REGISTRATION NUMBER: 26581
; REFERENCE/DOCKET NUMBER: 9437/3433
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3067
; TELEFAX: 202-822-0944

TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 345 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-792-259-12

Query Match 1.3%; Score 7; DB 1; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 463 SLIPPG 469
Db 152 SLIPPG 158

RESULT 55
US-08-997-803-14
Sequence 14, Application US/08997803
Patent No. 6057126
GENERAL INFORMATION:
APPLICANT: CHUN, Terold J. M.
APPLICANT: GUPPA, Ashwani
APPLICANT: MONROE, Donald G.
APPLICANT: VYAS, Tejal B.
TITLE OF INVENTION: MAMMALIAN EDG-5 RECEPTOR HOMOLOGS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mikaido, Marmelstein, Murray & Oram LLP
STREET: 655 Fifteenth Street, N.W., Suite 330
City: Washington
STATE: D. C.
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,803
FILING DATE: 24-DEC-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Wong, King L.
REGISTRATION NUMBER: 37,500
REFERENCE/DOCKET NUMBER: P8074-7020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-5000
TELEFAX: (202) 638-4810
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-997-803-14

Query Match 1.3%; Score 7; DB 3; Length 353;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 331 GLVVLPL 337
Db 255 GLVVLPL 261

RESULT 56
US-08-458-023B-6
Sequence 6, Application US/08458023B

Patent No. 5667990
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Yoder, Wendy
APPLICANT: Takagi, Shinobu
APPLICANT: Boonathnan, Karuppan C.
TITLE OF INVENTION: ASPERGILLUS EXPRESSION SYSTEM
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 56679900 No. 5667990disk of No. 5667990th America, Inc.
STREET: 405 Lexington Avenue
City: New York
STATE: New York
COUNTRY: USA
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,023B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lowmey Dr., Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4086.010-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 363 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-458-023B-6

Query Match 1.3%; Score 7; DB 1; Length 363;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 463 SLIPPG 469
Db 170 SLIPPG 176

RESULT 57
US-07-792-259-17
Sequence 17, Application US/07792259
Patent No. 5286638
GENERAL INFORMATION:
APPLICANT: TANAKA, YOSHIKAZU
APPLICANT: ASHIKARI, TOSHITAKO
APPLICANT: HATANAKA, HARUYO
APPLICANT: SHIBANO, YUJI
APPLICANT: AWACHI, TERUO
APPLICANT: NAKAYAMA, TORU
APPLICANT: SUMIDA, MOTOO
TITLE OF INVENTION: PEROXIDE GENE OF MICROBIAL ORIGIN
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1615 L. STREET, N.W.
City: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/792,259
FILING DATE: 1991115
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26581
REFERENCE/DOCKET NUMBER: 9437/93433
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3067
TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 364 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-792-259-17

Query Match 1.3%; Score 7; DB 1; Length 364;
Best Local Similarity 100.0%; Pred. No. 2.e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 463 SLIPPG 469
|||
DB 171 SLIPPG 177

RESULT 58
US-09-270-767-39038
Sequence 39038, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 39038
LENGTH: 383
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-39038

Query Match 1.3%; Score 7; DB 4; Length 383;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 LRSHRL 32
|||
DB 13 LRSHRL 19

RESULT 59
US-09-270-767-54255
Sequence 54255, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 54255

LENGTH: 383
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-54255

Query Match 1.3%; Score 7; DB 4; Length 383;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 LRSHRL 32
|||
DB 13 LRSHRL 19

RESULT 60
US-10-101-464A-902
Sequence 902, Application US/10101464A
Patent No. 6768041
GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions isolated from plant cells
TITLE OF INVENTION: and their use in the modification of plant cell signaling
FILE REFERENCE: 11000.1020C2
CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: PCT/US00/00724
PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 902
LENGTH: 386
TYPE: PRT
ORGANISM: Pinus radiata
US-10-101-464A-902

Query Match 1.3%; Score 7; DB 4; Length 386;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 351 SVLSLSA 357
|||
DB 277 SVLSLSA 283

RESULT 61
US-09-784-077-2
Sequence 2, Application US/09784077
Patent No. 6693183
GENERAL INFORMATION:
APPLICANT: NATSUKA, SHUNJI
APPLICANT: GERSTEN, KEVIN M.
TITLE OF INVENTION: MURINE ALPHA (1,3) FUCOSYLTRANSFERASE
FUC-TVII, DNA ENCODING THE SAME, METHOD FOR PREPARING THE
SAME, ANTIBODIES RECOGNIZING THE SAME, IMMUNOASSAYS FOR
DETECTING THE SAME, PLASMIDS CONTAINING SUCH DNA
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSER: OHION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA

COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/784,077
FILING DATE: 16-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/613,098
FILING DATE: 08-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: LAVALLEYE, JEAN-PAUL
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-114-55
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 393 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-784-077-2

Query Match 1.3%; Score 7; DB 4; Length 393;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RLRYRL 8
Db 355 RLRYRL 361

RESULT 62
US-08-845-381E-63
Sequence 63, Application US/08845381E
Patent No. 6602681
GENERAL INFORMATION:
APPLICANT: OHSUYE, Kazuhiro
APPLICANT: KITANO, Katsuhiko
APPLICANT: TANAKA, Shoji
APPLICANT: MATSUO, Hisayuki
APPLICANT: MIZONO, Kensaku
TITLE OF INVENTION: RECOMBINANT C-TERMINAL ALPHA-AMIDATING
TITLE OF INVENTION: ENZYME
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATTHEWS, L.L.P.
STREET: 1737 King Street, Suite 500
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22314-2756
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,381E
FILING DATE: 25-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 62177184
FILING DATE: 17-JUL-1987
PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 62306867
FILING DATE: 05-DEC-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/219,375
FILING DATE: 15-JUL-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/509,583
FILING DATE: 16-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Dadio, Susan M.
REGISTRATION NUMBER: 40,373
REFERENCE/DOCKET NUMBER: 001560-296
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: protein
US-08-845-381E-63

Query Match 1.3%; Score 7; DB 4; Length 400;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 NIPSSD 92
Db 111 NIPSSD 117

RESULT 63
US-08-289-222E-3
Sequence 3, Application US/08289222E
Patent No. 6120760
GENERAL INFORMATION:
APPLICANT: HOTTEN, GERTRUD
APPLICANT: NEIDHARDT, HELGE
APPLICANT: BECHTOLD, ROLF
APPLICANT: POHL, JENS
TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS OF THE TGF- β
TITLE OF INVENTION: FAMILY
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIKO, MARKELSTEIN, MURRAY & ORAM
STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
SUITE 330
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/289,222E
FILING DATE: 25-AUG-1999
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,222
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 23 190.3
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EPO 92102324.8
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00350

FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, MONICA CHIN
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P564-9021
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-289-222B-3

Query Match 1.3%; Score 7; DB 3; Length 401;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 346 LLDVRSV 352
Db 177 LLDVRSV 183

RESULT 64
US-09-054-526B-3
Sequence 3, Application US/09054526B
Patent No. 6197550
GENERAL INFORMATION:
APPLICANT: H. TEN, GERTTUD
APPLICANT: NEIDHARDT, HELGE
APPLICANT: BECHTOLD, ROLF
APPLICANT: BOHL, JENS
TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL
TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIKO, MARWELSTEIN, MURRAY & ORAM LLP
STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
STREET: SUITE 330
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/054,526B
FILING DATE: 03-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,222
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 23 190.3
FILING DATE: 01-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EPO 92102324.8
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00350
FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, MONICA CHIN
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P564-8005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-054-526B-3

Query Match 1.3%; Score 7; DB 3; Length 401;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 346 LLDVRSV 352
Db 177 LLDVRSV 183

RESULT 65
US-09-516-143A-2
Sequence 2, Application US/09516143A
Patent No. 6333182
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Human Glycosylation Enzymes
FILE REFERENCE: PF505PCT
CURRENT APPLICATION NUMBER: US/09/516,143A
CURRENT FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/122,409
PRIOR FILING DATE: 1999-03-02
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 434
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: 133
OTHER INFORMATION: Xaa equals Tyr or His
NAME/KEY: SITE
LOCATION: 136
OTHER INFORMATION: Xaa equals Gly or Val
NAME/KEY: SITE
LOCATION: 147
OTHER INFORMATION: Xaa equals Ser or Pro
NAME/KEY: SITE
LOCATION: 169
OTHER INFORMATION: Xaa equals Gly or Val
US-09-516-143A-2

Query Match 1.3%; Score 7; DB 3; Length 434;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 508 RPSRGP 514
Db 18 RPSRGP 24

RESULT 66
US-09-984-205-2
Sequence 2, Application US/09984205
Patent No. 6783971
GENERAL INFORMATION:
APPLICANT: Coleman, Timothy A. et al.
TITLE OF INVENTION: Human Glycosylation Enzymes
FILE REFERENCE: PF505D1
CURRENT APPLICATION NUMBER: US/09/984,205
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: PCT/US00/05325
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 09/516,143

PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/122,409
PRIOR FILING DATE: 1999-03-02
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 434
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: 133
OTHER INFORMATION: Xaa equals Tyr or His
NAME/KEY: SITE
LOCATION: 136
OTHER INFORMATION: Xaa equals Gly or Val
NAME/KEY: SITE
LOCATION: 147
OTHER INFORMATION: Xaa equals Ser or Pro
NAME/KEY: SITE
LOCATION: 169
OTHER INFORMATION: Xaa equals Gly or Val
US-09-984-205-2

Query Match 1.3%; Score 7; DB 4; Length 434;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 508 RPSRGP 514
DB 18 RPSRGP 24

RESULT 67
US-08-331-515A-2
Sequence 2, Application US/08331515A
Patent No. 5851811
GENERAL INFORMATION:
APPLICANT: Wellinder, Karen
TITLE OF INVENTION: PEROXIDASE VARIANTS WITH IMPROVED
TITLE OF INVENTION: HYDROGEN PEROXIDE STABILITY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSEE: No. 5851811 No. 5851811disk of No. 5851811th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,515A
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 3769,204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 435 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-331-515A-2

Query Match 1.3%; Score 7; DB 2; Length 435;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 463 SLIPGP 469
DB 171 SLIPGP 177

RESULT 68
US-09-168-406A-2
Sequence 2, Application US/09168406A
Patent No. 6258769
GENERAL INFORMATION:
APPLICANT: Wellinder, Karen G.
TITLE OF INVENTION: Peroxidase Variants With Improved
TITLE OF INVENTION: Hydrogen Peroxidase Stability
FILE REFERENCE: 3769,214-US
CURRENT APPLICATION NUMBER: US/09/168,406A
CURRENT FILING DATE: 1998-10-06
PRIOR APPLICATION NUMBER: 08/331,515
PRIOR FILING DATE: 1994-11-01
PRIOR APPLICATION NUMBER: PCT/DK93/00189
PRIOR FILING DATE: 1993-06-01
PRIOR APPLICATION NUMBER: 0792/92
PRIOR FILING DATE: 1992-06-01
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 435
TYPE: PRT
ORGANISM: Coprinus cinereus
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(435)
OTHER INFORMATION: Xaa = Any Amino Acid
US-09-168-406A-2

Query Match 1.3%; Score 7; DB 3; Length 435;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 463 SLIPGP 469
DB 171 SLIPGP 177

RESULT 69
US-09-198-452A-7
Sequence 7, Application US/09198452A
Patent No. 6559294
GENERAL INFORMATION:
APPLICANT: Griffiths, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 7
LENGTH: 460
TYPE: PRT
ORGANISM: Chlamydia pneumoniae
US-09-198-452A-7

Query Match 1.3%; Score 7; DB 4; Length 460;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 LOCKSRL 307

Db 292 LOKLSRL 298

RESULT 70
US-09-351-150A-9
; Sequence 9, Application US/09351150A
; Patent No. 653817
; GENERAL INFORMATION:
; APPLICANT: Davick, J
; TITLE OF INVENTION: Compositions and Methods for Fumonisin Detoxification
; FILE REFERENCE: 035718/167676, 5718-62
; CURRENT APPLICATION NUMBER: US/09/351,150A
; CURRENT FILING DATE: 1998-07-12
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Bacterium 2412.1
US-09-351-150A-9

Query Match 1.3%; Score 7; DB 4; Length 468;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 196 NDALIVL 202
Db 246 NDALIVL 252

RESULT 71
US-09-252-991A-24392
; Sequence 24392, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24392
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24392

Query Match 1.3%; Score 7; DB 4; Length 476;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 GDEETLA 64
Db 448 GDEETLA 454

RESULT 72
US-09-252-991A-27516
; Sequence 27516, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27516
; LENGTH: 477
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27516

Query Match 1.3%; Score 7; DB 4; Length 477;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 375 LYLRDFR 381
Db 233 LYLRDFR 239

RESULT 73
US-09-134-000C-5553
; Sequence 5553, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5553
; LENGTH: 477
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-5553

Query Match 1.3%; Score 7; DB 4; Length 477;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 185 TLYQSAD 191
Db 33 TLYQSAD 39

RESULT 74
US-09-252-991A-23317
; Sequence 23317, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23317
; LENGTH: 481
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23317

Query Match 1.3%; Score 7; DB 4; Length 481;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 508 RPSRGRP 514
Db 145 RPSRGRP 151

RESULT 75
US-08-455-559-10
; Sequence 10, Application US/08455559
; Patent No. 5801014
; GENERAL INFORMATION:
; APPLICANT: LEE, SE-JIN
; APPLICANT: HUYNH, THANH
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,559
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/003,144
; FILING DATE: 12-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WETHERILL, JR. PH.D., JOHN R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: PD2280
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/455-5100
; TELEFAX: 619-455-5110
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 495 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-455-559-10

Query March 1.3%; Score 7; DB 1; Length 495;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 346 LLDVRSV 352
Db 271 LLDVRSV 277

Search completed: November 16, 2004, 07:31:38
Job time : 43 secs

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